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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:14:51 ; Search time 47.9085 Seconds

(without alignments)  
1433.128 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSAGSVKL.....CMQGTHTSPITFGAGTKLEIK 243

Scoring table: BLOSUM62

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1289	100.0	243	2	AAW60769
2	1277	99.1	535	2	AAW28491
3	1277	99.1	535	2	AAW28492
4	985.5	76.5	353	2	AAW06273
5	970.5	75.3	257	3	AAW09777
6	961	74.6	249	2	AAW60770
7	930.5	72.2	238	5	AAW25963
8	930.5	72.2	238	5	AAW74420
9	930.5	72.2	238	6	AAW26732
10	926.5	71.9	240	5	AAW25960
11	926.5	71.9	240	5	AAW74419
12	926.5	71.4	253	5	ABP45953
13	920.5	71.4	253	5	ABP45953
14	918.5	71.3	241	7	AAW25961
15	913	70.8	238	5	ADD31766
16	911	70.7	281	2	AAW82744
17	911	70.7	666	2	AAW82745
18	908	70.4	240	7	ADD31769
19	906	70.3	270	4	AAW75719
20	902	70.0	251	4	AAW75719
21	902	70.0	556	4	AAW80040
22	902	70.0	556	4	AAW97935
23	900.5	69.9	271	3	AAW23818
24	900.5	69.9	271	4	AAW67494
25	900.5	69.9	271	5	AAW47632

26	900.5	69.9	271	5	ABG97809	ABG97809 Mouse MAB
27	900.5	69.9	271	5	ABG35312	ABG35312 Thrombopo
28	900.5	69.9	274	3	AAW23817	AAW23817 Plasmid p
29	900.5	69.9	274	4	AAW67493	AAW67493 Amino aci
30	900.5	69.9	274	5	AAW47631	AAW47631 Murine MA
31	900.5	69.9	274	5	ABG97808	ABG97808 Mouse MAB
32	900.5	69.9	274	5	ABG35311	ABG35311 Thrombopo
33	900.5	69.8	553	2	AAW11508	AAW11508 Single ch
34	900	69.8	553	4	AAW73223	AAW73223 H22-anti-
35	900	69.8	553	4	AAW61960	AAW61960 Bispectifi
36	900	69.8	553	4	AAW85455	AAW85455 Bispectifi
37	895.5	69.5	249	1	AAW80154	AAW80154 Biosynthe
38	892.5	69.2	245	4	AAW67498	AAW67498 Murine aci
39	892.5	69.2	245	5	AAW47636	AAW47636 Murine MA
40	892.5	69.2	245	5	ABG35316	ABG35316 Thrombopo
41	892.5	69.2	271	3	AAW23820	AAW23820 Plasmid p
42	892.5	69.2	271	4	AAW67496	AAW67496 Amino aci
43	892.5	69.2	271	5	AAW47634	AAW47634 Murine MA
44	892.5	69.2	271	5	ABG97811	ABG97811 Mouse MAB
45	892.5	69.2	271	5	ABG97811	ABG97811 Mouse MAB

## ALIGNMENTS

## RESULT 1

AAW60769 standard; protein; 243 AA.

AAW60769;

08-SEP-1998 (first entry)

Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.

Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;

regulatory domain; p53 mutant; H273; W248; G281;

p53-dependent trans-activating activity; restoration;

tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;

cancer; re-stenosis; ss.

Mus sp.

27-OCT-1997; 97WO-FR001921.

29-OCT-1996; 96FR-00013176.

(RHON ) RHONE-POULENC RORER SA.

Bracco L, Debussche L;

WPI: 1998-272140/24.

N-PSDB; AAW36236.

Restoring p53-dependent trans-activating activity to cell containing

mutant p53 - by delivering single-chain antibody specific for the mutant,

particularly for treatment of tumours.

Claim 5; Page 31; 54pp; French.

The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53-dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation

CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53

XX Sequence 243 AA;

Query Match 100.0%; Score 1289; DB 2; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-83;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSASVLTSLTASGFNTKDYIMHWKORPEQGLMIGMIDPENGDTEY 60  
 DB 1 QVQLQSGAEIVRSASVLTSLTASGFNTKDYIMHWKORPEQGLMIGMIDPENGDTEY 60  
 QY 61 APPEQKAMTADTSNTAVIQLSLASEDTAVYYCNFYGDALDYWGQGTITVSSGGGG 120  
 DB 61 APPEQKAMTADTSNTAVIQLSLASEDTAVYYCNFYGDALDYWGQGTITVSSGGGG 120  
 QY 121 SGGGSGGGGSDVLMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSP 180  
 DB 121 SGGGSGGGGSDVLMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSP 180  
 QY 181 KRLLIVSKLDSGVPPRFSGSGGTPFTLKINVEAEDLGYYCMQGTHSPLTFGAGTKL 240  
 DB 181 KRLLIVSKLDSGVPPRFSGSGGTPFTLKINVEAEDLGYYCMQGTHSPLTFGAGTKL 240  
 QY 241 EIK 243  
 DB 241 EIK 243

# RESULT 2

AAW28491  
 ID AAW28491 standard; protein; 535 AA.

XX AAW28491;

DT 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325 encoded by p53176.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; re-stenosis; SCFV;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.

XX Homo sapiens.  
 OS Herpes simplex virus.  
 OS Synthetic.  
 OS Chimeric.

XX MO9704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR001111.

XX 19-JUL-1995; 95FR-00008729.

XX (RHON) RHONE POULENC RORER SA.

XX Conseller E, Bracco L;

XX MPI; 1997-132633/12.

XX N-PSDB; AAT86221.

XX New p53 variants e.g. with oligomerisation domain replaced by leucine  
 PT zipper - useful for treating hyper-proliferative disorders, esp. cancer  
 PT and re-stenosis.

XX Claim 36; Page 88-90; 133pp; French.

XX Claimed variants of protein p53 have at least part of the oligomerisation

CC domain deleted and replaced by a leucine zipper domain. The mutants  
 CC preferably also have at least part of the p53 transactivation domain  
 CC (amino acids 1-74) deleted and replaced by the transactivating domain  
 CC (TAD) from herpes simplex virus viral protein VP16 (amino acids 411-490)  
 CC or by a protein domain able to bind selectively to a transactivator.  
 CC especially a single-chain antibody variable domain (SCFV). The present  
 CC sequence is that of a specifically claimed p53 variant designated S-325  
 CC and comprising a SCFV domain, amino acids 75-325 of human wild-type p53  
 CC and a leucine zipper domain at the C-terminal. The p53 variants are more  
 CC active and more stable tumour suppressors and apoptosis-inducing agents  
 CC than wild-type p53 and are active where the wild-type protein is not,  
 CC i.e. they are not inactivated by dominant negative or oncogenic mutants,  
 CC nor by other cellular proteins (because the leucine zipper domain  
 CC prevents formation of inactive mixed oligomers)

XX Sequence 535 AA;

Query Match 99.1%; Score 1277; DB 2; Length 535;  
 Best Local Similarity 98.8%; Pred. No. 2.1e-82;  
 Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSASVLTSLTASGFNTKDYIMHWKORPEQGLMIGMIDPENGDTEY 60  
 DB 3 QVQLQSGAEIVRSASVLTSLTASGFNTKDYIMHWKORPEQGLMIGMIDPENGDTEY 62  
 QY 61 APPEQKAMTADTSNTAVIQLSLASEDTAVYYCNFYGDALDYWGQGTITVSSGGGG 120  
 DB 63 APPEQKAMTADTSNTAVIQLSLASEDTAVYYCNFYGDALDYWGQGTITVSSGGGG 122  
 QY 121 SGGGSGGGGSDVLMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSP 180  
 DB 123 SGGGSGGGGSDVLMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSP 182  
 QY 181 KRLLIVSKLDSGVPPRFSGSGGTPFTLKINVEAEDLGYYCMQGTHSPLTFGAGTKL 240  
 DB 183 KRLLIVSKLDSGVPPRFSGSGGTPFTLKINVEAEDLGYYCMQGTHSPLTFGAGTKL 242  
 QY 241 EIK 243  
 DB 243 EIK 245

# RESULT 3

AAW28492  
 ID AAW28492 standard; protein; 535 AA.

XX AAW28492;

DT 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325H.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; re-stenosis; SCFV;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.

XX Homo sapiens.  
 OS Herpes simplex virus.  
 OS Synthetic.  
 OS Chimeric.

XX Key

XX Misc-difference 361

XX W09704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR001111.

Location/Qualifiers  
 /note= "Arg residue at position 182 of wild-type p53 has  
 been mutated to His"

XX	Mus sp		Location/Qualifiers
OS	Synthetic.		1..21
OS	Chimeric.		/note= "Ig K-chain SP"
FT	Peptide	22..30	/note= "HA epitope"
FT	Domain	38..160	/note= "A77 VL"
FT	Peptide	161..175	/note= "linker"
FT	Domain	176..287	/note= "A77 VH"
FT	Peptide	294..303	/note= "Myc epitope"
FT	Domain	304..353	/note= "PDGFR transmembrane domain"
PX	MO3928349-A2.		
PD	10-JUN-1999.		
PX	02-DEC-1998;	98WO-US025556.	
PR	02-DEC-1997;	97US-0067232P.	
PA	(MEDA-) MEDAREX INC.		
PI	Keller T, Goldstein J, Graziano R, Deo YM,		
DR	WPI; 1999-371099/31.		
DX	N-PDB; AAX58936.		
PT	Cells expressing anti-Fc receptor binding components.		
PS	Example 6; Fig 10A-E; 68pp; English.		
CC	The present sequence represents a fusion protein comprising murine anti-		
CC	Fc alpha receptor antibody A77 sfv and the transmembrane domain of		
CC	platelet derived growth factor receptor (PDGF-R TM). It is encoded by		
CC	c expression vector pUG718 (see AAX58935). Murine tumour cells transformed		
CC	to express A77-TM were able to bind a soluble form of the Fc alpha		
CC	receptor, and the bound receptor was able to engage IgA molecules. This		
CC	is an example of cells of the invention that have been transformed to		
CC	express on their surface a component which binds to an Fc receptor of an		
CC	effector cell. The transformed cell is targeted to an effector cell via		
CC	the Fc binding component, and can be used as a vehicle to increase an		
CC	phagocytosis, against an antigen associated with the cell. The		
CC	transformed cells are used to treat cancer and infectious diseases or		
CC	used as vaccines. The method allows for killing of target cells without		
CC	tagging any particular antigen on the cell. This is advantageous since		
CC	many tumour cells and other target cells do not have defined antigens for		
CC	targeting		
XX	Sequence 353 AA:		
QY	Query Match	76.5%; Score 985.5; DB 2; Length 353;	
Db	Best Local Similarity	75.2%; Pred. No. 6e-62;	
Matches	188; Conservative	23; Mismatches	32; Indels
1	QVQLQQSGAEIVRSGASVLTCTASGAFNIKDYMAHWVKORPEQGLEIWTGMIDPENGDTEY	60	
38	EIQDQQTGEILVPKAGSVNISCKAGSYFTYLITIFWVKSQHSKLEIWTGNNNPYGGSITSY	97	
61	APFQQAAMTADTSNTAYQLSSIASEDFAVYC-----NFYG----DALDYWGQGTVT	113	
98	NKEKKAKLTLTYDKSSSTAHYNMLNLTJESDAVVYICRGVGYTSSSTEAFPIYWGGGLTVT	157	

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Db      158 VSAGGGGGGGGGGGGGVVTQTPLTLITIGQPASISCKSSQSLDSDKTYLNMLL 217
QY      174 QRPQSPKRLIYLVSKLDSGVDPDRFTSGSGGDTFTLKINRVEADLGVYVCWGTHSPLT 233
Db      218 QRPQSPKRLIYLVSKLDSGVDPDRFTSGSGGDTFTLKISRVEADLGVYVCWGTHSPOT 277
QY      234 FGAGTYLLEIK 243
Db      278 FGAGTYLLEIK 287

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## RESULT 5

AAB09777 standard; protein; 257 AA.

AAB09777; 06-SEP-2000 (first entry)

Anti-viral scFv-antibody against the 3a movement protein of CMV.

Molecular pathogenicity; plant disease; resistance; antibody; scFv; gene construct; pathogen; toxin; fusion protein; antimicrobial; deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.

Tobacco mosaic virus.  
Human herpesvirus 5.

WO200023593-A2.

27-APR-2000.

15-OCT-1999; 99WO-EP007844.

16-OCT-1998; 98EP-00119630.  
16-OCT-1998; 98IN-MU000666.

(FRAU) FRAUNHOFER GES FORDERUNG ANGEWANDTEN.

Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y, Spiegel H, Zimmerman S, Emsan N, Holzem A;

WPI; 2000-339692/29.

New fusion proteins and gene constructs for expressing agents (antibodies, enzymes, vectors or molecular pathogenicity), useful for protecting plants against pathogens and increasing resistance to disease.

Example 6; Fig 23a; 193pp; English.

The present invention describes a fusion protein (I) comprising at least one binding domain specifically recognising an epitope of a plant pathogen and at least one further domain comprising a protein or peptide sequence which is toxic to the pathogen or detrimental to its replication, transmission or life cycle. Also described is a pathogenicity (II) comprising (I) and a cellular targeting sequence and/or membrane localisation sequence and/or motif that leads to membrane anchoring or at least one binding domain that specifically recognises a viral movement and/or replicase protein. The fusion protein, pathogenicity, polynucleotide, vectors, and compositions from the present invention are useful for the protection of a plant against the action of a pathogen. The kit from the present invention is useful for carrying out the methods and may be employed in different applications, for example in the diagnostic field or as research tools. The kit or its components, such as the fusion protein, pathogenicity, polynucleotides, vectors or compositions are useful in plant cell and plant tissue culture, in agriculture. They are extremely useful for breeding new varieties of plants that display improved properties such as resistance to pathogens. AA656587 to AA656702 and AAB09774 to B097820 represent sequences used in the exemplification of the present invention

Sequence 257 AA;

Query Match 75.3%; Score 970.5; DB 3; Length 257;

Best Local Similarity 77.2%; Pred. No. Se-61; Mismatches 33; Indels 11; Gaps 3;

Matches 193; Conservative 13; Mismatches 33; Indels 11; Gaps 3;

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QY      1 QYOLQSGAGELVRSASVYLSCTASGFNFKDYMHMVKRQPEGLMTGIDPENGDIEY 60
Db      3 EYQLOQSGAGELVRSASVYLSCTASGFNFKDYMHMVKRQPEGLMTGIDPENGDIEY 62
QY      61 APRFOGKATMTDVTSSNTNRYLDLSSLASHPDVAVYVCNFFGDLADYWGQGTWTVSAGG- 119
Db      63 NQKFKGKATLTADKSSITAYWQJLSITSEDSAVYYC---APPDVGAGTLLIFVSAGAP 118
QY      120 ---GSG---GGSGGGGGSDVLTMTQPLTLITSVITIGQPASISCKSSQSLDSDKTYLNMLL 173
Db      119 TSGSGKPGPGEGSTKCAPVYLTQAPLTLITSVITIGQPASISCKSSQSLDSDKTYLNMLL 178
QY      174 QRPQSPKRLIYLVSKLDSGVDPDRFTSGSGGDTFTLKINRVEADLGVYVCWGTHSPLT 233
Db      179 QRPQSPKRLIYLVSKLDSGVDPDRFTSGSGGDTFTLKISRVEADLGVYVCWGTHSPHT 238
QY      234 FGAGTYLLEIK 243
Db      239 FGAGTYLLEIK 248

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## RESULT 6

AAM60770 standard; protein; 249 AA.

AAM60770;

08-SEP-1998 (first entry)

Single chain antibody (ScFv) D3M that binds to mutant p53 proteins.

Single chain antibody; scFv D3M; mouse; p53 protein; oligomerisation; regulatory domain; p53 mutant; H273; W248; G281; p53-dependent trans-activating activity; restoration; tumour-suppressing activity; tumour cell; treatment; hyper-proliferation; cancer; re-stenosis; ss.

Mus sp.

WO9818625-A1.

07-MAY-1998.

27-OCT-1997; 97WO-FR001921.

29-OCT-1996; 96FR-00013176.

(RHON) RHONE-POULENC RORER SA.

Bracco I, Debussche J;

WPI; 1998-272140/24.  
N-FSDB; AAV36237.

Restoring p53-dependent trans-activating activity to cell containing mutant p53 - by delivering single-chain antibody specific for the mutant, particularly for treatment of tumours.

Claim 5; Page 32; 54pp; French.

The present sequence represents a single chain antibody (ScFv) designated D3M. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically in positions 320 and 393. ScFv D3M is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53-dependent trans-activating activity is restored. ScFv D3M is specific for p53-mutants that have lost tumour-suppressing activity and are present in



CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53  
 XX  
 SQ Sequence 249 AA;

Query Match 74.6%; Score 961; DB 2; Length 249;  
 Best Local Similarity 74.8%; Pred. No. 2.3e-60;  
 Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

QY 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMMWVKQPEQGLEWIGIDPENGDTET 60  
 Db 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMMWVKQPEQGLEWIGIDPENGDTET 60  
 QY 61 APRFQKATMTADTSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTIVY 114  
 Db 61 APRFQKATMTADTSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTIVY 120  
 QY 115 SSGGGSGGGGGSGGSDVLTMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 173  
 Db 121 SSGGGSGGGGGSGGSDVLTMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 180  
 QY 174 QRGSGPKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILT 233  
 Db 181 QRGSGPKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILT 239  
 QY 234 FGAGTLEIK 243  
 Db 240 FGAGTLEIK 249

RESULT 7  
 AAE25963  
 ID AAE25963 standard; protein; 238 AA.  
 AC AAE25963;

DT 15-NOV-2002 (first entry)  
 DE KDR binding immunoglobulin related mouse protein #3.

KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
 KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
 KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
 KW p1C11; scFv antibody.

OS Mus sp.

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-00976787.

PR 28-JAN-2000; 2000US-00493539.

PA (ZHUZ/) ZHU Z.

PA (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase  
 XX insert domain-containing receptor with an affinity comparable to human  
 XX vascular endothelial growth factor, and neutralizes activation of KDR.

PS Disclosure; Page 17-18; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind  
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable

CC to human vascular endothelial growth factor (VEGF) and that neutralises  
 CC activation of KDR. Sequences of the invention are useful for neutralising  
 CC the activation of KDR, for reducing tumour growth and for inhibiting  
 CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
 CC mouse protein  
 XX  
 SQ Sequence 238 AA;

Query Match 72.2%; Score 930.5; DB 5; Length 238;  
 Best Local Similarity 71.7%; Pred. No. 3.1e-58;  
 Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

QY 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMMWVKQPEQGLEWIGIDPENGSDY 60  
 Db 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMMWVKQPEQGLEWIGIDPENGSDY 60  
 QY 61 APRFQKATMTADTSNTAVYLTQSLASEDTAVYYCN-FYGDALDYMGGQTIVYSSGG 119  
 Db 61 APRFQKATMTADTSNTAVYLTQSLASEDTAVYYCNFYGMWVKQPEQGLEWIGIDPENGSDY 120  
 QY 120 GSGGGSGGGGGSGGSDVLTMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 179  
 Db 121 GSGGGSGGGGGSGGSDVLTMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 174  
 QY 180 PKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILTFAGTK 239  
 Db 175 PKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILTFAGTK 234  
 QY 240 LEIK 243  
 Db 235 LEIK 238

RESULT 8  
 AAU74420  
 ID AAU74420 standard; protein; 238 AA.  
 AC AAU74420;

DT 26-MAR-2002 (first entry)

DE Antigen-binding protein, single chain variable fragment version #2.

KW Antigen-binding protein; single chain variable fragment; scFv; antigen;  
 KW cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
 KW vascular endothelial growth factor receptor; VEGF;  
 KW cell proliferation inhibitor.

OS Mus sp.

OS Synthetic.

PH Key Location/Qualifiers

FT Region 1..117 /label= VH

FT /note= "Heavy chain variable domain. Specifically claimed in claim 61"

FT Region 118..132 /label= Linker

FT /note= "15 amino acid linker joins the VH and VL regions of the single chain variable fragment protein. Encoded by AAS20285"

FT Region 133..238 /label= VL

FT /note= "Light chain variable domain. Specifically claimed in claim 61"

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016924.

PR 24-MAY-2000; 2000US-0206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.  
 PA  
 XX  
 XX

Zhu Z;

WPI; 2002-106189/14.

New bispecific immunoglobulin-like antigen-binding protein for reducing tumor growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides.

Claim 63; Page 62-63; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a  
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
 CC are stably associated in an immunoglobulin like complex. P1 has an  
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
 CC light chain constant domain (CL domain), and P2 has an antigen-binding  
 CC site located to the N terminus of the CH1 domain. (I) is useful for:  
 CC neutralising the activation of a vascular endothelial growth factor  
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
 CC reducing endothelial cell proliferation; inhibiting VEGF induced  
 CC migration of human leukaemia cells; blocking interaction of a protein and  
 CC its ligand; promoting interactions between immune cells and target cells;  
 CC and in vivo and in vitro for investigative, diagnostic or treatment  
 CC methods. The design of (I) provides for efficient production so that  
 CC substantially all of the antigen-binding proteins produced are assembled  
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
 CC and in tetrameric form. The heavy chain constant domains which constitute  
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
 CC antibody and which provide other antibody functions can be present. There  
 CC is no requirement for processing in vitro to obtain the complete product.  
 CC This is the amino acid sequence of a single chain variable fragment  
 CC (scFv), an engineered protein containing a variable light and variable  
 CC heavy domain on one polypeptide, described in the method of the invention  
 CC  
 XX Sequence 238 AA;  
 SQ

Query Match 72.2%; Score 930.5; DB 5; Length 238;

Best Local Similarity 71.7%; Pred. No. 3,1e-58;  
 Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

```

QY 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGWIDPENGDTTEY 60
Db 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGWIDPENGSDY 60
QY 61 APRFOGKATMTADTSNTAYQLSLASEDTAVYYCN-FYGDALDYMGGGTTVTYSSGGG 119
Db 61 APRFOGKATMTADSSSNTAYQLSLTSEDTAVYYCNAYGDYSGWGGGTTVTYSSGGG 120
QY 120 GSGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNMLLQRPQS 179
Db 121 GSGGGSGGGSDIRLTQSPAIMSAPGKVTITCSASSV-----SYMWFQOKPETS 174
QY 180 PKRLIYVSKIDSGVPRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPILFGAGT 239
Db 180 PKRLIYVSKIDSGVPRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPILFGAGT 239
QY 175 PKLMTYSTNLASGVPAFSSGSGSTSYSLTISRVEADATYVCOQRRSYPTFTGSGTK 234
Db 175 PKLMTYSTNLASGVPAFSSGSGSTSYSLTISRVEADATYVCOQRRSYPTFTGSGTK 234
QY 240 LEIK 243
Db 240 LEIK 238

```

RESULT 9

ID ABL26732 standard; protein; 238 AA.

ABJ26732;

01-MAY-2003 (first entry)

VEGF binding related protein SEQ ID No 28.

XX

KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
 KM leukaemia cell; vascular endothelial growth factor; tumour;  
 XX bispecific antigen-binding protein; mouse; murine.

OS Mus sp.

XX WO2003002144-A1.

XX 09-JAN-2003.

XX 26-JUN-2002; 2002WO-US020332.

XX 26-JUN-2001; 2001US-0301299P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z;

XX WPI; 2003-201468/19.

XX New bispecific antibodies having antigen-binding sites specific for a  
 PT first vascular endothelial growth factor (VEGF) receptor and for a second  
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for  
 PT treating tumors.  
 XX  
 PS Disclosure; Page 56-57; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding  
 CC site specific for a first vascular endothelial growth factor (VEGF)  
 CC receptor and a second antigen-binding site specific for a second VEGF  
 CC receptor. The bispecific antigen-binding proteins block activation of the  
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
 CC cellular functions such as mitogenesis of vascular endothelial cells and  
 CC migration of leukemia cells. The antibodies are useful for treating  
 CC tumours and for in vivo or in vitro for investigative and diagnostic  
 CC methods. This sequence represents a mouse protein relating to the  
 CC bispecific antibodies that bind to the VEGF receptors of the invention  
 CC  
 XX Sequence 238 AA;  
 SQ

Query Match 72.2%; Score 930.5; DB 6; Length 238;

Best Local Similarity 71.7%; Pred. No. 3,1e-58;  
 Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

```

QY 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGWIDPENGDTTEY 60
Db 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGWIDPENGSDY 60
QY 61 APRFOGKATMTADTSNTAYQLSLASEDTAVYYCN-FYGDALDYMGGGTTVTYSSGGG 119
Db 61 APRFOGKATMTADSSSNTAYQLSLTSEDTAVYYCNAYGDYSGWGGGTTVTYSSGGG 120
QY 120 GSGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNMLLQRPQS 179
Db 121 GSGGGSGGGSDIRLTQSPAIMSAPGKVTITCSASSV-----SYMWFQOKPETS 174
QY 180 PKRLIYVSKIDSGVPRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPILFGAGT 239
Db 180 PKRLIYVSKIDSGVPRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPILFGAGT 239
QY 175 PKLMTYSTNLASGVPAFSSGSGSTSYSLTISRVEADATYVCOQRRSYPTFTGSGTK 234
Db 175 PKLMTYSTNLASGVPAFSSGSGSTSYSLTISRVEADATYVCOQRRSYPTFTGSGTK 234
QY 240 LEIK 243
Db 240 LEIK 238

```

RESULT 10

ID AAE25960 standard; protein; 240 AA.

AAE25960;

15-NOV-2002 (first entry)

XX

DE KDR binding immunoglobulin related mouse protein #1.  
 XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
 XX foetal liver kinase; Flk-1 receptor; vascular endothelial growth factor;  
 KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
 KW pIC11; scfv antibody.  
 XX Mus sp.  
 XX US2002064528-A1.  
 PN 30-MAY-2002.  
 PD 12-OCT-2001; 2001US-00976787.  
 PF 28-JAN-2000; 2000US-00493539.  
 PR (ZHUZ/) ZHU Z.  
 PA (WITT/) WITTE L.  
 XX ZHU Z, Witte L;  
 PI ZHU Z, Witte L;  
 PT WPI; 2002-589175/63.  
 DR N-PADB; AAD42824.  
 XX  
 PS Disclosure; Page 16-17; 34pp; English.  
 CC The present invention relates to novel immunoglobulin molecules that bind  
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
 CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable  
 CC to human vascular endothelial growth factor (VEGF) and that neutralises  
 CC activation of KDR. Sequences of the invention are useful for neutralising  
 CC the activation of KDR, for reducing tumour growth and for inhibiting  
 CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
 CC mouse protein  
 XX  
 SQ Sequence 240 AA;  
 Query Match 71.9%; Score 926.5; DB 5; Length 240;  
 Best Local Similarity 71.7%; Pred. No. 6.1e-58;  
 Matches 175; Conservative 26; Mismatches 36; Indels 7; Gaps 2;  
 QY 1 QVQLQSGAEIVRSGSVKLSCTASGPNIKDYIMENVKQRPQGLFMTGMDPENGDTRY 60  
 Db 1 QVRLQSGAEIVSGASVRLSCTTSGFNTKDFPMHVKORPQGLEMTGMDPENGDGTY 60  
 QY 61 AEFQGGKATMTADTSNTAYLQLSSLASDPAVYYCN-FYGDALDYWGQGTVTYSSGGG 119  
 Db 61 AEFQGGKATMTADTSNTAYLQLSSLASDPAVYYCN-FYGDALDYWGQGTVTYSSGGG 120  
 QY 120 GGGGGGGGGGGSDVMTQCTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLQRPQGS 179  
 Db 121 GGGGGGGGGGGSDIETLQSPAIMSASPGKXVITCSASSV-----SYMHEFQCKPGTS 174  
 QY 180 PRLILYVSKLDSGPDRTSGSGDPTLKTNRLEARDLVYYCMQGHSLTTCAGTK 239  
 Db 175 PRLILYVSKLDSGPDRTSGSGDPTLKTNRLEARDLVYYCMQGHSLTTCAGTK 234  
 QY 240 LEIK 243  
 Db 235 LEIK 238  
 RSSTT 11  
 ID AAV74419 standard; protein; 240 AA.  
 XX AAV74419;  
 XX

DT 26-MAR-2002 (first entry)  
 XX  
 DE Antigen-binding protein, single chain variable fragment version #1.  
 XX  
 KW Antigen-binding protein; single chain variable fragment; scfv; antigen;  
 KW cytostatic; angiogenesis inhibitor; tumour; leukemia; antibody;  
 KW vascular endothelial growth factor receptor; VEGF;  
 KW cell proliferation inhibitor.  
 XX  
 XX Mus sp.  
 OS Synthetic.  
 OS  
 FH Key  
 FT Region  
 FT Location/Qualifiers  
 FT 1..117  
 FT /label= VH  
 FT /note="Heavy chain variable domain. Specifically claimed  
 FT in claim 57"  
 FT 118..132  
 FT /label= linker  
 FT /note="15 amino acid linker joins the VH and VL regions  
 FT of the single chain variable protein. Encoded by  
 FT AAS20285"  
 FT 133..240  
 FT /label= VL  
 FT /note="light chain variable domain. Specifically claimed  
 FT in claim 57"  
 PN WO200190192-A2.  
 XX 29-NOV-2001.  
 PD 24-MAY-2001; 2001WO-US016924.  
 XX 24-MAY-2000; 2000US-0206749P.  
 XX (IMC-) IMCLONE SYSTEMS INC.  
 PA ZHU Z;  
 PI ZHU Z;  
 XX WPI; 2002-106189/14.  
 DR  
 XX  
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two  
 PT polypeptides and two second polypeptides.  
 PS  
 PS Claim 63; Page 62; 64pp; English.  
 CC The invention describes an antigen-binding protein (I) comprising a  
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
 CC are stably associated in an immunoglobulin like complex. P1 has an  
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
 CC light chain constant domain (CL domain), and P2 has an antigen-binding  
 CC site located to the N terminus of the CH1 domain. (I) is useful for:  
 CC neutralising the activation of a vascular endothelial growth factor  
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
 CC reducing endothelial cell proliferation; inhibiting VEGF induced  
 CC migration of human leukemia cells; blocking interaction of a protein and  
 CC its ligand; promoting interactions between immune cells and target cells;  
 CC and in vivo and in vitro for investigative, diagnostic or treatment  
 CC methods. The design of (I) provides for efficient production so that  
 CC substantially all of the antigen-binding proteins produced are assembled  
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
 CC and in tetrameric form. The heavy chain constant domains which constitute  
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural  
 CC antibody and which provide other antibody functions can be present. There  
 CC is no requirement for processing in vitro to obtain the complete product.  
 CC This is the amino acid sequence of a single chain variable fragment  
 CC (scfv), an engineered protein containing a variable light and variable  
 CC heavy domain on one polypeptide, described in the method of the invention  
 XX  
 SQ Sequence 240 AA;  
 Query Match 71.9%; Score 926.5; DB 5; Length 240;

Best Local Similarity 71.7%; Pred. No. 6.1e-58; Matches 175; Conservative 26; Mismatches 36; Indels 7; Gaps 2;

```

QY 1 QVQLQSGAEIVRSASVLTCTASGFNIDKYYMHVWKRPQGLEWIGMIDPENGDTEY 60
D 1 QVQLQSGAEIVRSASVLTCTASGFNIDKYYMHVWKRPQGLEWIGMIDPENGDSCY 60
QY 61 APKFGKATMTADTSNTAYLQLSLASDPAVYYCN-FYGDALDYGGGTTVYSSGGG 119
D 61 APKFGKATMTADSSNTAYLQLSLASDPAVYYCNAYGDEYGGGTTVYSSGGG 120
QY 120 GSGGGSGGGSDVLTQTPPLTISVTIGQPASISCKSSQSLDSDGTYLNMILLQRPQGS 179
D 121 GSGGGSGGGSDVLTQTPPLTISVTIGQPASISCKSSQSLDSDGTYLNMILLQRPQGS 174
QY 180 PKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPITFGAGTK 239
D 175 PKLMIYSTSNLASGVDPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPITFGAGTK 234
QY 240 LEIK 243
D 235 LEIK 238

```

RESULT 12  
ABJ26731  
ID ABJ26731 standard; protein; 240 AA.  
XX  
AC ABJ26731;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE VEGF binding related protein SEQ ID No 27.

XX Cytostratic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
XX leukaemia cell; vascular endothelial growth factor; tumour;  
XX bispecific antigen-binding protein; mouse; murine.

XX Mus sp.

PN W02003002144-A1.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US020332.

PR 26-JUN-2001; 2001US-0301299P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2003-201468/19.

XX New bispecific antibodies having antigen-binding sites specific for a  
XX first vascular endothelial growth factor (VEGF) receptor and for a second  
XX VEGF receptor, useful for inhibiting migration of leukemia cells, or for  
XX treating tumors.

PS Disclosure; Page 55-56; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding  
XX site specific for a first vascular endothelial growth factor (VEGF)  
XX receptor and a second antigen-binding site specific for a second VEGF  
XX receptor. The bispecific antigen-binding proteins block activation of the  
XX VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
XX cellular functions such as mitogenesis of vascular endothelial cells and  
XX migration of leukaemia cells. The antibodies are useful for treating  
XX tumours and for in vivo or in vitro for investigative and diagnostic  
XX methods. This sequence represents a mouse protein relating to the  
XX bispecific antibodies that bind to the VEGF receptors of the invention

XX Sequence 240 AA;

Query Match 71.9%; Score 926.5; DB 6; Length 240;  
Best Local Similarity 71.7%; Pred. No. 6.1e-58; Matches 175; Conservative 26; Mismatches 36; Indels 7; Gaps 2;

```

QY 1 QVQLQSGAEIVRSASVLTCTASGFNIDKYYMHVWKRPQGLEWIGMIDPENGDTEY 60
D 1 QVQLQSGAEIVRSASVLTCTASGFNIDKYYMHVWKRPQGLEWIGMIDPENGDSCY 60
QY 61 APKFGKATMTADTSNTAYLQLSLASDPAVYYCN-FYGDALDYGGGTTVYSSGGG 119
D 61 APKFGKATMTADSSNTAYLQLSLASDPAVYYCNAYGDEYGGGTTVYSSGGG 120
QY 120 GSGGGSGGGSDVLTQTPPLTISVTIGQPASISCKSSQSLDSDGTYLNMILLQRPQGS 179
D 121 GSGGGSGGGSDVLTQTPPLTISVTIGQPASISCKSSQSLDSDGTYLNMILLQRPQGS 174
QY 180 PKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPITFGAGTK 239
D 175 PKLMIYSTSNLASGVDPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPITFGAGTK 234
QY 240 LEIK 243
D 235 LEIK 238

```

RESULT 13  
ABP45953  
ID ABP45953 standard; protein; 253 AA.

XX ABP45953;

DT 19-AUG-2002 (first entry)

XX Human BlyS binding scFv SEQ ID 1964.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostratic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

PN W0200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PI WPI; 2002-114799/15.

XX Antbodies against B lymphocyte Stimulating polypeptides, useful for the  
XX diagnosis and treatment of cancers and immune disorders.  
XX  
XX Claim 1; Page 2744-2745; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
XX B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
XX tumour necrosis factor (TNF) super family and induces B cell  
XX proliferation and differentiation. The antibodies of the invention have

CC cytostatic immunosuppressive, immunostimulant, immunomodulatory,  
CC antithematic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blyss. The antibodies bind to Blyss  
CC and so may be used to detect and quantitate the presence of Blyss in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blyss. They may also be  
CC administered to treat diseases associated with aberrant Blyss expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
Sequence 253 AA;  
SQ

Sequence 253 AA;

Query Match	71.4%	Score 920.5;	DB 5;	Length 253;
Best Local Similarity	70.2%	Pred. No. 1.7e-57;		
Matches 177;	Conservative	26;	Mismatches 40;	Indels 9;
			Gaps	3

QY	QVQLQSGAEIVSGASVTLCTASGSENIKCYMHMWVQRPEGLGEMTGLMDPENGDTEY	60
Db	QVQLQSGAEIVSGASVTLCTASGSENIKCYMHMWVQRPEGLGEMTGLMDPENGDTEY	60
QY	1 QVQLQSGAEIVSGASVTLCTASGSENIKCYMHMWVQRPEGLGEMTGLMDPENGDTEY	60
Db	1 QVQLQSGAEIVSGASVTLCTASGSENIKCYMHMWVQRPEGLGEMTGLMDPENGDTEY	60
QY	61 APFPGKATMTADTSSNTAYTLQSLASHEDTAVYCC--NFYGDA----LDYWGQGTYYT	113
Db	61 APFPGKATMTADTSSNTAYTLQSLASHEDTAVYCC--NFYGDA----LDYWGQGTYYT	113
QY	114 VSSGGSGSGSGSGSGSGSG--DYLMNTQPTLLSYTTCGPASISCSKSSQSGLSDSDGKTYLAW	171
Db	114 VSSGGSGSGSGSGSGSGSG--DYLMNTQPTLLSYTTCGPASISCSKSSQSGLSDSDGKTYLAW	171
QY	121 VSSGGSGSGSGSGSGSGSG--DYLMNTQPTLLSYTTCGPASISCSKSSQSGLSDSDGKTYLAW	180
Db	121 VSSGGSGSGSGSGSGSGSG--DYLMNTQPTLLSYTTCGPASISCSKSSQSGLSDSDGKTYLAW	180
QY	172 LLOPFGQSPRRLLIYLVSKLDSGVPRFTFGSGSGTDFTLKINRVAEADIGVYVCMQGTISP	231
Db	172 LLOPFGQSPRRLLIYLVSKLDSGVPRFTFGSGSGTDFTLKINRVAEADIGVYVCMQGTISP	231
QY	181 FOORFPGQSPRRLLIYLVSKLDSGVPRFTFGSGSGTDFTLKINRVAEADIGVYVCMQGTISP	240
Db	181 FOORFPGQSPRRLLIYLVSKLDSGVPRFTFGSGSGTDFTLKINRVAEADIGVYVCMQGTISP	240
QY	232 LTFGAGTKLEIK 243	
Db	232 LTFGAGTKLEIK 243	
QY	241 FTFGQGTMEIK 252	
Db	241 FTFGQGTMEIK 252	

```
RESULT 14
AAE25961
ID AAE25961 standard; protein; 238 AA
vv
```

DT 15-NOV-2002 (first entry)  
 DT 15-NOV-2002 (first entry)

KDR binding immunoglobulin related mouse protein #2.

KM mouse; immunoglobulin; kinase insert domain-containing receptor; KDR,  
KM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor,  
KM VEGF; tumour growth; heavy-chain variable region; VH, angiogenesis;  
KM p1C11, scFv antibody.

Mus sp. - OS

PN US2002064528-A1

PD 30-MAY-2002.

12-OCT-2001; 2001US-00976787.

28-JAN-2000; 2000US-00493539.

PA (ZHUZ/) ZHU Z.  
PA (WITTE/) WITTE T

XX  
PT 7h11 7 11:11 = 1

XX  
WPB, 2003 E9017F

DR N-PSDB; AAD42825.

XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase  
PT insert domain-containing receptor with an affinity comparable to human  
PT vascular endothelial growth factor, and neutralizes activation of KDR.  
XX  
PS Disclosure; Page 17-18; 34pp; English.  
XX

The present invention relates to novel immunoglobulin molecules that bind to kinase insert domain-containing receptor (KDR) (a human homologue of mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable to human vascular endothelial growth factor (VEGF) and that neutralises activation of KDR. Sequences of the invention are useful for neutralising the activation of KDR, for reducing the tumour growth and for inhibiting angiogenesis. The present sequence is KDR binding immunoglobulin related mouse protein.

Sequence 238 AA;

Query March	71.3%	Score 918.5	DB 5	Length 238
Best Local Similarity	70.9%	Pred. No. 2.2e-57		
Matches 173	Conservative 27	Mismatches 30	Indels 7	Gaps 2

[illegible]

RESULT 15  
ADD31766  
ID ADD31766 standard; protein; 241 AA.  
y

DT 15-JAN-2004 (first entry)  
 YY

DE Anti-CEA single chain monoclonal antibody C50 protein SEQ ID NO:5.

anti-CEA single chain monoclonal antibody.

OS Synthetic.

PN WO2003064611-A2  
XY

PD 07-AUG-2003.  
yy

29-JAN-2003; 2003WO-US002612.

PR 30-JAN-2002; 2002US--00062188.  
YY

PA (EGEA-) EGEA BIOSCIENCES INC.

PI Evans GA;  
YY

WPI; 2003-663477/62.  
N-PSDB: ADD3176E



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:17:36 ; Search time 14.3232 Seconds  
(without alignments)  
875.861 Million cell updates/sec

Title: US-09-297-181-2  
Perfect score: 1289  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	99.1	535	US-08-983-035A-38	Sequence 38, Appl
2	985.5	76.5	353	US-09-203-958A-4	Sequence 4, Appl
3	911	70.7	281	US-09-423-439-44	Sequence 44, Appl
4	911	70.7	666	US-09-423-439-51	Sequence 51, Appl
5	906	70.3	270	US-08-652-507-2	Sequence 2, Appl
6	900	69.8	553	US-08-661-052-16	Sequence 16, Appl
7	900	69.8	553	US-08-188-082-16	Sequence 16, Appl
8	900	69.8	553	US-09-364-088-16	Sequence 16, Appl
9	900	69.8	553	US-09-102-716-16	Sequence 16, Appl
10	866	67.2	348	US-09-646-028-12	Sequence 12, Appl
11	866	67.2	361	US-09-646-028-14	Sequence 14, Appl
12	843.5	65.4	288	US-09-423-439-38	Sequence 38, Appl
13	843.5	65.4	288	US-08-184-658-63	Sequence 63, Appl
14	843.5	65.4	289	US-09-504-262D-63	Sequence 63, Appl
15	843.5	65.4	673	US-09-423-439-32	Sequence 32, Appl
16	829	64.3	248	US-09-649-063-23	Sequence 23, Appl
17	828.5	64.3	247	US-09-227-693-34	Sequence 34, Appl
18	828.5	64.3	248	US-08-331-398A-34	Sequence 34, Appl
19	828.5	64.3	248	US-08-331-397B-34	Sequence 34, Appl
20	828.5	64.3	248	US-08-759-804A-34	Sequence 34, Appl
21	815.5	63.0	281	US-08-875-811-53	Sequence 178, App
22	812	63.0	365	US-08-875-811-53	Sequence 53, Appl
23	812	63.0	366	US-09-070-408-132	Sequence 132, App
24	809.5	62.4	239	US-08-279-772A-8	Sequence 8, Appl
25	804	62.4	239	US-08-902-486-11	Sequence 11, Appl
26	804	62.4	239	US-08-902-486-11	Sequence 11, Appl
27	804	62.4	599	US-08-463-163-3	Sequence 3, Appl

28	801.5	62.2	263	US-08-752-844-66	Sequence 66, Appl
29	801.5	62.2	263	US-09-293-533-66	Sequence 66, Appl
30	798.5	61.9	260	US-08-447-402-1	Sequence 1, Appl
31	798	61.9	240	US-10-092-246-36	Sequence 36, Appl
32	795.5	61.7	240	US-10-092-246-37	Sequence 37, Appl
33	795.5	61.7	246	US-08-257-341-7	Sequence 7, Appl
34	795.5	61.7	252	US-08-133-804-4	Sequence 4, Appl
35	795.5	61.7	252	US-08-461-838-4	Sequence 4, Appl
36	795.5	61.7	252	US-08-461-838-4	Sequence 4, Appl
37	795.5	61.7	367	US-08-257-341-5	Sequence 5, Appl
38	791.5	61.4	244	US-09-244-369B-1	Sequence 1, Appl
39	785	60.9	269	US-08-646-265A-109	Sequence 109, App
40	784	60.8	240	US-10-092-246-35	Sequence 35, Appl
41	780.5	60.6	268	US-09-554-765-2	Sequence 2, Appl
42	780.5	60.6	408	US-09-554-765-15	Sequence 15, Appl
43	780.5	60.6	409	US-09-554-765-14	Sequence 14, Appl
44	776.5	60.2	249	US-08-797-689-18	Sequence 18, Appl
45	776.5	60.2	249	US-09-984-186-18	Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-08-983-035A-38  
Sequence 38, Application US//08983035A  
Patent No. 6326464  
GENERAL INFORMATION:  
APPLICANT: CONSEILLER, EMMANUEL  
BRACCO, LAURENT  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
US25 THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DONNER, LLP  
STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentm Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US//08/983,035A  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-983-035A-38  
Query Match 99.1%; Score 1277; DB 4; Length 535;  
Best local Similarity 98.8%; Pred. No. 6,8e-95;

Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGIDPENGDTEY 60  
Db 3 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGIDPENGDTEY 62

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCNFYGALDYWGQGTIVTVSSGGGG 120  
Db 63 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCNFYGALDYWGQGTIVTVSSGGGG 122

QY 121 SGGGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLMLQRPQSP 180  
Db 123 SGGGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLMLQRPQSP 182

QY 181 KRLIIVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYVCWQGTSPFTGAGTKL 240  
Db 183 KRLIIVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYVCWQGTSPFTGAGTKL 242

QY 241 EIK 243  
Db 243 EIK 245

RESULT 2  
US-09-203-958A-4  
Sequence 4, Application US/09203958A  
Patent No. 6682928  
GENERAL INFORMATION:  
APPLICANT: KELLER, Tibor  
APPLICANT: GOLDSTEIN, Joel  
APPLICANT: GRAZIANO, Robert  
APPLICANT: DEO, Yashwant M.  
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR  
TITLE OF INVENTION: BINDING COMPONENTS  
FILE REFERENCE: MXI-099CPA  
CURRENT APPLICATION NUMBER: US/09/203,958A  
CURRENT FILING DATE: 1998-12-02  
PRIOR APPLICATION NUMBER: 60/067232  
FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-09-203-958A-4

Query Match 76.5%; Score 985.5; DB 4; Length 353;  
Best Local Similarity 75.2%; Pred. No. 1.1e-71;  
Matches 188; Conservative 23; Mismatches 32; Indels 7; Gaps 2;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGIDPENGDTEY 60  
Db 38 EIQQLQTEPELVKPKASVYKISCKASGVFTDYIIIFWQSHKLEWVGNNPPYGSTSY 97

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCNFYG--DALDYWGQGTIVT 113  
Db 98 NLKFKGKATLTIVDKSSSTAYVQNLNLSLSEDSAVVYCVAGVYVYGGSYEAFFWGGTIVT 157

QY 114 VSSGGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLML 173  
Db 158 VSAAGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLML 217

QY 174 QRPQSPKRLIIVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYVCWQGTSPFT 233  
Db 218 QRPQSPKRLIIVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYVCWQGTSPFT 277

QY 234 FGAGTKLEIK 243  
Db 278 FGAGTKLEIK 287

RESULT 3  
US-09-423-439-44  
Sequence 44, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
APPLICANT: BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-09-423-439-44

Query Match 70.7%; Score 911; DB 4; Length 281;  
Best Local Similarity 70.4%; Pred. No. 8.3e-66;  
Matches 174; Conservative 27; Mismatches 36; Indels 10; Gaps 3;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGIDPENGDTEY 60  
Db 23 EVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGIDPENGDTEY 82

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCN--FYGD--ALDYWGQGTIVTVSS 116  
Db 83 APRKQGRATMTADPSSNTAYIHLSLSASEDTAVYYCHVLIAGLIAMDYWGQGTIVTVSS 142

QY 117 GGGGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLMLQRP 176  
Db 143 GGGGSGGGGSDVMTQPTLTSLVITIGQPASISCKSSQSLSDSDGKTYLMLQRP 196

QY 177 GQSPKRLIIVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYVCWQGTSPFT 236  
Db 197 GTSPEKMTYSTSLNLSGVPAFSSGSGTSTLTISRMEADDAITYQQRSTYPLTFGA 256

QY 237 GTKLEIK 243  
Db 257 GTKLEIK 263

RESULT 4  
US-09-423-439-51  
Sequence 51, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
APPLICANT: BLAKEY, David Charles



```

/ TITLE OF INVENTION: CHEMICAL COMPOUNDS
/
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Pillebury Winthrop, L.L.P.
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MS Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/423 439
/ FILING DATE: 09-NO. 6339070-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GH98/01294
/ FILING DATE: 05-MAY-1998
/ APPLICATION NUMBER: GB 9709421.3
/ FILING DATE: 10-MAY-1997
/
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 666 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

```

```

Query Match          70.7%; Score 911; DB 4; Length 666;
Best Local Similarity 70.4%; Pred. No. 2,2e-65;
Matches 174; Conservative 27; Mismatches 36; Indels 10; Gaps 3;

QY 1 QVQLQSGAEIVRSAGSVKLSCTASGFNPKDYMMHWKORPEQGLMIGMIDPENDDEX 60
DB 20 EVQLQSGAEIVRSAGSVKLSCTASGFNPKDMHWKORPEQGLMIGMIDPENDDEX 79
QY 61 ARPGQKATMTADTSNTAYLQLSLASEDTAVYYCN--FYGD--ALDYGQGTIVT 116
DB 80 ARPGQKATMTADTSNTAYLHLSLTSRDTAVYYCHVLIVAGYLAAMDYWGQTSVAVSS 139
QY 117 GGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLLQRP 176
DB 140 GGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLLQRP 193
QY 177 GQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOQTHSPITFGA 236
DB 194 GTSPKLMIYSTNLSAGVAPARFGSGSGTSYSTLTIRMAEDDAATYYCOQRSTYPLTFGA 253
QY 237 GTKLRLK 243
DB 254 GTKLRLK 260

```

```

RESULT 5
US-08-652-507-2
/ Sequence 2, Application US/08652507
/ Patent No. 5876691
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Nixon & Vanderhye, P.C.
/ STREET: 1100 No. 5876691th Glebe Road, 8th Floor
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: USA

```

```

/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/652,507
/ FILING DATE: 02-JUL-1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arthur R. Crawford
/ REGISTRATION NUMBER: 25,327
/ REFERENCE/DOCKET NUMBER: 117-211
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-816-4000
/ TELEFAX: 703-816-4100
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 270 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-652-507-2

```

```

Query Match          70.3%; Score 906; DB 2; Length 270;
Best Local Similarity 69.2%; Pred. No. 2e-65;
Matches 173; Conservative 26; Mismatches 35; Indels 16; Gaps 3;

QY 1 QVQLQSGAEIVRSAGSVKLSCTASGFNPKDYMMHWKORPEQGLMIGMIDPENDDEX 60
DB 27 QVQLQSGAEIVRSAGSVKLSCTASGFNPKDYMMHWKORPEQGLMIGMIDPENDDEX 86
QY 61 ARPGQKATMTADTSNTAYLQLSLASEDTAVYYCN-----FYGDALDYGQGTIVT 113
DB 87 ARPGQKATMTADTSNTAYLHLSLTSRDTAVYYCNEGTPGPPY---FDYWGQGTIVT 143
QY 114 VSSGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLL 173
DB 144 VSSGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLL 197
QY 174 QRPQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOQTHSPIT 233
DB 198 QRPQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOQTHSPIT 257
QY 234 FGAGTKLRLK 243
DB 258 FGAGTKLRLK 267

```

```

RESULT 6
US-08-661-052-16
/ Sequence 16, Application US/08661052
/ Patent No. 5837243
/ GENERAL INFORMATION:
/ APPLICANT: Yashwant M. Deo
/ APPLICANT: Joel Goldstein
/ APPLICANT: Robert Graziano
/ APPLICANT: Chezia Somasundaram
/ TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISHD
/ TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street, Suite 510
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS

```



Query Match	69.8%;	Score 900;	DB 4;	Length 553;
Best Local Similarity	68.7%;	Pred. No. 1.4e-64;		
Matches 171;	Conservative 27;	Mismatches 35;	Indels 16;	Gaps 3

RESULT 9  
US-09-102-716-16  
; Sequence 16, Application US/09102716  
; Patent No. 6395272

Ubel Goldstein  
Robert Graziano

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISE  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESS: LARIVE & COCKFIELD  
STREET: 60 State Street, Suite 5100  
CITY: BOSTON, MA 02109

STATE: Massachusetts

ZIP: 02109-1875

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102,716

FILING DATE: 22-Jun-1998  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052  
FILING DATE: <Unknown>

NAME: Arnold, Beth E.

Query Match	69.8%	Score 900;	DB 4;	length 553;
Best Local Similarity	68.7%;	Pred. No. 1.4e-64;		
Matches 171;	Conservative 27;	Mismatches 35;	Indels 16;	Gaps 3;

RESULT 10  
US-09-646-028-12  
; Sequence 12, Application US/09646028  
; Patent No. 6562347

APPLICANT: Kwak, Larry

TITLE OF INVENTION: METH

FILE REFERENCE: 14014.0316/P

: CURRENT FILING DATE: 2000-09-12  
 : PRIOR APPLICATION NUMBER: 60/073 745

PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12

```

```

; LENGTH: 348
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct

Query Match

Best local similarity 65.3%; Fred. NO. 4.4e-62;  
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1.

QY 1 QV0LOS6AE1VRSGAVKLSCTASGENTKDYMHMWK0PDE0GLEWIGWIDPENGDTXY 60

Db 98 EVQLQSGSPDLVKPGMSVKLSCKTGYNFSDKRIHWIKQKPGRGLEWVGRIIDPSNGDTDY 157

61 APKFGKATMTADTSSNTAYLQLSSASEDTAVYYCNFYGD--ALDYWGCGTIVTVSSGG 118

```

Db      158 NADFKTPATLTVDRPSNTAYLEISNLTSGDAVYYCSIGDYACDIWGCGTETLVSSG 217
QY      119 GSGGGGGGGGGGSDVMTQPTLTLSVTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 178
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      218 GSGGGGGGGGGGSDVMTQPTLTLSVSLGPHVMSCRQNSLVNSHGDSFLHMFLOKPG 277
QY      179 SPKRLIYVSKLDSGVPDRFTSGSGTDFTLKINRYEADLGYIYCCGTHSPITGAGT 238
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      278 SPKRLIYKVSRRPFVPERFSGSGTDFTLISRVEADLGYVFCQGAHVEMTFGGGT 337
QY      239 KLEIK 243
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      338 KLEVK 342

```

```

RESULT 11
US-09-646-028-14
; Sequence 14, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biraqyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct
US-09-646-028-14

```

```

Query Match      67.2%; Score 866; DB 4; Length 361;
Best Local Similarity 65.3%; Pred. No. 4.6e-62;
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

QY      1 QVQLQSGAEIVRSQASVKLSCTASGNIKDYMMHWKQRPQGLEWIGMIDPENGTREY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      111 EVQLQSGPDLVYKPGMSVKLSCKTLGYNFSDKRIMHMKQKRGSLIEWVGRIDPSNGDTDY 170
QY      61 APRKQKATMTADTSSNTAYLQLSLSLASEDTAVYYCNFYPD--ALDYWGQGTITVYSSGG 118
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      171 NADPKTPATLTVDRPSNTAYLEISNLTSGDAVYYCSIGDYACDIWGCGTETLVSSGG 230
QY      119 GSGGGGGGGGGGSDVMTQPTLTLSVTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 178
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      231 GSGGGGGGGGGGSDVMTQPTLTLSVSLGPHVMSCRQNSLVNSHGDSFLHMFLOKPG 290
QY      179 SPKRLIYVSKLDSGVPDRFTSGSGTDFTLKINRYEADLGYIYCCGTHSPITGAGT 238
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      291 SPKRLIYKVSRRPFVPERFSGSGTDFTLISRVEADLGYVFCQGAHVEMTFGGGT 350
QY      239 KLEIK 243
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      351 KLEVK 355

```

```

RESULT 12
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen Charles
; APPLICANT: Blakey, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

```

```

Query Match      65.4%; Score 843.5; DB 4; Length 288;
Best Local Similarity 66.3%; Pred. No. 2.3e-60;
Matches 165; Conservative 31; Mismatches 46; Indels 7; Gaps 3;

QY      1 QVQLQSGAEIVRSQASVKLSCTASGNIKDYMMHWKQRPQGLEWIGMIDPENGTREY 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      23 QVQLQSGAEIVRSQASVKLSCTASGNYFTGWIMHWKQRPQGLEWIGVNSTGRSDY 82
QY      61 APRKQKATMTADTSSNTAYLQLSLSLASEDTAVYYC-----NFGDMLDYWGQGTITVVS 115
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      83 NEKFKNATLTIVKSSSTTAAWQLSLSEDSAVYYCARERAYGYDDMDYWGQGTITVVS 142
QY      116 SGGGGGGGGGGGSDVMTQPTLTLSVTIGQPASISCKSSQSLNDSGKTYLWMLQ 174
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      143 SGGGGGGGGGGGSDVMTQPTLTLSVSLGPHVMSCRQNSLVNSHGDSFLHMFLOKPG 202
QY      175 RPQSPKRLIYVSKLDSGVPDRFTSGSGTDFTLKINRYEADLGYIYCCGTHSPITF 234
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      203 RPQSPKRLIYMASTRFTSGVDPDRFTSGSGTDFTLTISVOAEDLAIYYCKQ--SYLRTF 261
QY      235 GAGTKLEIK 243
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      262 GGGTKLEIK 270

```

```

RESULT 13
US-09-184-658-63
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Olteneess, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69

```

```

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: pcANTAB6 signal peptide; Val at position 1 is most
OTHER INFORMATION: likely initiator Met.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (23)..(138)
OTHER INFORMATION: 5109 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (139)..(154)
OTHER INFORMATION: 16 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
FEATURE:
NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER INFORMATION: myc tag.
FEATURE:
NAME/KEY: SITE
LOCATION: (284)..(289)
OTHER INFORMATION: His tag.
US-09-184-658-63

```

```

Query Match      65.4%; Score 843.5; DB 3; Length 289;
Best Local Similarity 68.4%; Pred. No. 2.3e-60;
Matches 167; Conservative 23; Mismatches 53; Indels 1; Gaps 1;

```

```

QY 1 OVQLQSGAEIVRSASVYKLSCTASGFNFKDYMHVQRPQGLWIMIDPENGDPTX 60
DB 23 EVQLVESGGSGVQPGSLKLSCTASGFTFNNTYGMGHWRTQPKRLIEWATINSNGLTIFY 82
QY 61 APEFGKATMTADTSNSTAYIQLSLASEDTAVYYCNFYGDALDYWGQGTVTVSSGGGG 120
DB 83 ADSVKGFTISRDNKNTLYIQMNRKSGDSGMYYCVRGYSNVARWGQALVTSSGGGG 142
QY 121 SGGGGSGGGG-SDVIMTQTPLTSLTTIGQPASISCKSSQSILDSGKTYLNLQRPQGS 179
DB 143 SGGGGSGGGGSDVIMTQTPLTSLTTIGQPASISCKSSQSILDSGKTYLNLQRPQGS 202
QY 180 PKRLIIVSKLDSGVDPDRFTSGSGSDPTLTKINRYEAEDELGYVYCMOGTHSPLTGAGTK 239
DB 203 PKRLIIVSELDSDVPDRFTSGSGSDPTLTKISRAEADLVGYVCCQGTHPHTGAGTK 262
QY 240 LEIK 243
DB 263 LEIK 266

```

```

RESULT 14
US-09-504-262D-63
Sequence 63, Application US/09504262D
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Salterelli, Mary J.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
FILE REFERENCE: PC10189GPR - CIP of PC9946A
CURRENT APPLICATION NUMBER: US/09/504,262D
CURRENT FILING DATE: 2000-02-15

```

```

NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5109 scFv from clone p5109C scFv7
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL scFv.
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: pcANTAB6 signal peptide; Val at position 1 is most likely initi
OTHER INFORMATION: or Met.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (23)..(138)
OTHER INFORMATION: 5109 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (139)..(154)
OTHER INFORMATION: 16 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
FEATURE:
NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER INFORMATION: myc tag.
FEATURE:
NAME/KEY: SITE
LOCATION: (284)..(289)
OTHER INFORMATION: His tag.
US-09-504-262D-63

```

```

Query Match      65.4%; Score 843.5; DB 4; Length 289;
Best Local Similarity 68.4%; Pred. No. 2.3e-60;
Matches 167; Conservative 23; Mismatches 53; Indels 1; Gaps 1;

```

```

QY 1 OVQLQSGAEIVRSASVYKLSCTASGFNFKDYMHVQRPQGLWIMIDPENGDPTX 60
DB 23 EVQLVESGGSGVQPGSLKLSCTASGFTFNNTYGMGHWRTQPKRLIEWATINSNGLTIFY 82
QY 61 APEFGKATMTADTSNSTAYIQLSLASEDTAVYYCNFYGDALDYWGQGTVTVSSGGGG 120
DB 83 ADSVKGFTISRDNKNTLYIQMNRKSGDSGMYYCVRGYSNVARWGQALVTSSGGGG 142
QY 121 SGGGGSGGGG-SDVIMTQTPLTSLTTIGQPASISCKSSQSILDSGKTYLNLQRPQGS 179
DB 143 SGGGGSGGGGSDVIMTQTPLTSLTTIGQPASISCKSSQSILDSGKTYLNLQRPQGS 202
QY 180 PKRLIIVSKLDSGVDPDRFTSGSGSDPTLTKINRYEAEDELGYVYCMOGTHSPLTGAGTK 239
DB 203 PKRLIIVSELDSDVPDRFTSGSGSDPTLTKISRAEADLVGYVCCQGTHPHTGAGTK 262
QY 240 LEIK 243
DB 263 LEIK 266

```

```

RESULT 15
US-09-423-439-32
Sequence 32, Application US/09423439
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BIAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:

```

ADDRESSER: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32

Query Match 65.4%; Score 843.5; DB 4; Length 673;  
Best Local Similarity 66.3%; Pred. No. 6e-60; Indels 7; Gaps 3;  
Matches 165; Conservative 31; Mismatches 46;

QY 1 QVQLQSGAEIVSGASVKSCTASGFINIKDYWMHWKQRPQOGLWIGWIDPENGDTTEY 60  
20 QVQLQSGAEIVSGASVKSCTASGFINIKDYWMHWKQRPQOGLWIGWIDPENGDTTEY 79  
61 APRKQKATMTADTSSNTAYLQLSLASEDTAVYYC-----NFGDALDYWGQGTIVTS 115  
80 NEKKNKATLTVDKSSSTAYMQLSLTSEDSAVYYCARERAYGYDAMDYWGQGTIVTS 139  
QY 116 SGSGSGSGSGSGSGSVLMTQTPLTSLVITIGQSPASISCKSSQSLIDS-DGKTYLAWLLQ 174  
140 SGSGSGSGSGSGSGSDIELSQSPSLAVSAGEKVTWSCSSQSLNSRTRKNYLAAYQQ 199  
QY 175 RFGQSPRLIYLVSKLDSGVDRFTSGSGSGDTFTLKINRYAEADLGYYCQGTSPPLTF 234  
200 RFGQSPRLIYLVSKLDSGVDRFTSGSGSGDTFTLKINRYAEADLGYYCQGTSPPLTF 258  
Db 235 GAGTKLEIK 243  
259 GAGTKLEIK 267

Search completed: July 30, 2004, 11:22:26  
Job time : 15.3232 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:36 ; Search time 13.3354 Seconds  
(without alignments)  
1752.823 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSGASVXL.....CWQGTSPILTFAGTLEIK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_78:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	912.5	70.8	249	2 S41374	single chain Fv an
2	832.5	64.6	233	2 JCS322	p53 specific singl
3	815	63.2	268	2 A56446	Ig heavy chain V r
4	560	43.4	132	2 C32513	Ig kappa chain pre
5	553	42.9	113	2 F30560	Ig kappa chain V r
6	545.5	42.3	136	2 S04576	Ig heavy chain pre
7	541	42.0	112	2 A55491	proteolytic antibo
8	539	41.8	112	2 A36259	Ig kappa chain V r
9	537	41.7	111	2 S20709	Ig kappa chain V r
10	528	41.0	116	2 S15672	Ig heavy chain V r
11	527	40.1	112	2 PL0273	Ig heavy chain V r
12	517	40.9	137	2 S52445	Ig heavy chain V r
13	511	39.6	101	2 A33730	Ig kappa chain V r
14	509.5	39.5	120	2 S03471	Ig heavy chain V-D
15	509	39.5	131	2 S31577	Ig kappa chain - m
16	505.5	39.2	118	2 S25174	Ig heavy chain V r
17	500	38.8	178	2 S29594	Ig gamma chain (WM
18	488	37.9	122	2 S06823	Ig heavy chain V r
19	487.5	37.8	117	2 S17586	Ig heavy chain V r
20	485.5	37.7	120	2 S03484	Ig heavy chain V-D
21	479.5	37.2	221	2 S49220	Ig gamma-1 chain -
22	476	36.9	133	2 S23330	Ig kappa chain pre
23	474	36.9	142	2 S22902	Ig kappa chain V r
24	475.5	36.8	116	2 S24289	Ig gamma chain V r
25	474.5	36.8	115	2 S03482	Ig heavy chain V-D
26	474	36.8	103	2 PH1055	Ig light chain V r
27	473	36.7	133	2 S42611	HUNWV protein prec
28	472	36.6	133	2 S40324	Ig kappa chain V r
29	471	36.5	108	2 PH1012	Ig heavy chain V r

30	469	36.4	91	2 S42186	Ig kappa chain V r
31	469	36.4	133	1 K2HURP	Ig kappa chain pre
32	468.5	36.3	140	2 S22658	Ig kappa chain pre
33	465	36.1	103	2 PH1056	Ig light chain V r
34	464.5	36.0	144	2 B30502	Ig heavy chain V r
35	463	35.9	118	2 S40374	Ig kappa chain - h
36	462	35.8	114	4 A47271	nitrophenyl phosph
37	461	35.8	133	1 A24452	Ig kappa chain pre
38	460.5	35.7	114	2 B49002	Ig kappa chain V r
39	460	35.7	112	2 A31807	Ig kappa chain V r
40	458.5	35.6	114	2 S49572	Ig kappa chain pre
41	453	35.1	122	2 S40338	Ig kappa chain - h
42	451	35.0	131	2 B39276	Ig light chain pre
43	450	34.9	115	2 S38715	Ig kappa chain V r
44	449	34.8	132	2 S40322	Ig kappa chain V r
45	447	34.7	112	2 S38719	Ig light chain V r

## ALIGNMENTS

## RESULT 1

S41374  
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A/Accession: S41374

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <ART>

A/Cross-references: EMBL:229480

## Query Match

Best Local Similarity 70.8%; Score 912.5; DB 2; Length 249;

Matches 179; Conservative 25; Mismatches 38; Indels 5; Gaps 2;

QY	1	QVQLQSGAEIVRSGASVXLCTASGFNIDYMMHWVKRPEQGLRWIGMDENGDT	60
DB	1	QVQLQSGAEIVRSGASVXLCTASGFNIDYMMHWVKRPEQGLRWIGMDENGDT	60
QY	61	AKRFQKATMTDTSNTYIQLSLASDITAVYC---NFGALDIWGGSTVTVSS	116
DB	61	VERFDKATITADTSNTYIQLSLASDITAVYC---NFGALDIWGGSTVTVSS	119
QY	117	GGGSGGGSGGGSDVMTQPTLTSTVITIGDPASTSCSSQSLSDSKTYINMLORP	176
DB	120	RGGSGGGSGGGSDVMTQPTLTSTVITIGDPASTSCSSQSLSDSKTYINMLORP	179
QY	177	GQSPKRLIYVSKLDSGVDPDRFTGSGSGTDFTLKINRVAEDLVGVVYCWQGTSP	236
DB	180	GQSPQLIYRMSNLASGVDRFSGSGSFTLRLSRVAEDLVGVVYCWQGTSP	239
QY	237	GTKLEIK 243	
DB	240	GTKLEIK 246	

RESULT 2  
p53 specific single-chain antibody Pab421 - human  
C/Species: Homo sapiens (man)  
C/Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
C/Accession: JCS322  
R/Darnault, C.B.; Hynes, N.E.  
Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  
A/Reference number: JCS322; MUID:97168950; PMID:9016757  
A/Accession: JCS322

A:Molecule type: mRNA  
 A:Residues: 1-233 <JAN>  
 A:Experimental source: hydriocoma cell  
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 64.6%; Score 832.5; DB 2; Length 233;  
 Best Local Similarity 68.9%; Pred. No. 4,4e-53;  
 Matches 164; Conservative 25; Mismatches 44; Indels 5; Gaps 3;

QY 5 QQSAGELVRSAGSVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTEYAPKF 64  
 DB 1 QESGAEIVRSAGSVKLSCTTSGFNINDYMHVWKORPEQGLEWIGRIDPENGDAMRRSS 60

QY 65 QGKATMTADTSSNTAYQLSSLSASEDTAVVYCNFYGDALDYGQCTTVTVSSGGSGSGG 124  
 DB 61 GYKATMTADTSSNTAYQLSSLSASEDTAVVYCN--AGMDYWGQCTTVTVSSGGSGSGGR 117

QY 125 GSGGGSDVLMQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSPKRLT 184  
 DB 118 ASGGGSDILTPSPALAVSLGQRAITSCASKS-VSTSGYSTMHMNQKRPQPPRLI 176

QY 185 YIVSKLDGVPDRFTSGSGTDFTLKINRYEADLGYVYCMQGTHSPLTGAGTKLEI 242  
 DB 177 YIVSNLESGVPARRSSGSGTDFTLNHPYREEDAAITYC-QHIRELTRESGGTXLEI 233

## RESULT 3

A56446  
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)  
 C>Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446  
 C/Tang, P.M.; Mahoney, W.C.; Foltz, L.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A:Reference number: A56446; MUID:9522583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 63.2%; Score 815; DB 2; Length 268;  
 Best Local Similarity 64.5%; Pred. No. 9.4e-52;  
 Matches 158; Conservative 30; Mismatches 49; Indels 8; Gaps 3;

QY 1 QVOIQSGAEIVRSAGSVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTEY 60  
 DB 3 QVKIQSGAEIVRSAGSVKLSCTTSGFNINDYMHVWKORPEQGLEWIGRIAPANGITKY 62

QY 61 APEQKATMTADTSSNTAYQLSSLSASEDTAVVYCNFYGDALD-YWGQCTTVTVSSGG 118  
 DB 63 DPKQKATMTADTSSNTAYQLSSLSASEDTAVVYCNFYGDALD-YWGQCTTVTVSSGG 122

QY 119 GSGGGSGSGSDVLMQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSG 178  
 DB 123 GSGGGSGSGSDILTPSPALAVSLGQRAITSCASKS-VSTSGYSTMHMNQKRPQPPRLI 176

QY 179 SPKRLIYVSKLDGVPDRFTSGSGTDFTLKINRYEADLGYVYCMQGTHSPLTGAGTK 238  
 DB 177 SPKRLIYVSKLDGVPDRFTSGSGTDFTLKINRYEADLGYVYCMQGTHSPLTGAGTK 236

QY 239 KLEIK 243  
 DB 237 KLEIK 241

## RESULT 4

C32513  
 Ig kappa chain precursor V region (BXW14) - mouse

C:Species: Mus musculus (house mouse)  
 C>Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C/Accession: C32513

R/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa 194c chain variable region gene complex organization and

A:Reference number: A94689; MUID:8831394; PMID:3138286

A/Accession: C32513

A:Molecule type: DNA

A:Residues: 1-132 <KOF>

A:Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/36-115/Domain: immunoglobulin homology <IM>

Query Match 43.4%; Score 560; DB 2; Length 132;  
 Best Local Similarity 95.5%; Pred. No. 1e-33;  
 Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 132 DVMTQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSPKRLIYVSKLD 191  
 DB 21 DVMTQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSPKRLIYVSKLD 80

QY 192 SGVPDRFTSGSGTDFTLKINRYEADLGYVYCMQGTHSPLTGAGTKLEI 243  
 DB 81 SGVPDRFTSGSGTDFTLKISRYEADLGYVYCMQGTHSPRTGGGTXLEI 132

## RESULT 5

F30560  
 Ig kappa chain V region (28.4.10A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000

C/Accession: F30560

R/Matsuda, T.; Kabat, E.A.

J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal

A:Reference number: A30560; MUID:89110062; PMID:2464028

A/Accession: F30560

A/Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/16-95/Domain: immunoglobulin homology <IM>

Query Match 42.9%; Score 553; DB 2; Length 113;  
 Best Local Similarity 94.6%; Pred. No. 2.8e-33;  
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 132 DVMTQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSPKRLIYVSKLD 191  
 DB 1 DVMTQTPPLTSTVIGQPASISCKSSQSLDSDGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVPDRFTSGSGTDFTLKINRYEADLGYVYCMQGTHSPLTGAGTKLEI 243  
 DB 61 SGVPDRFTSGSGTDFTLKISRYEADLGYVYCMQGTHSPRTGGGTXLEI 112

## RESULT 6

S04576  
 Ig heavy chain precursor V region (MR1-histone 7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000

C/Accession: S04576

R/Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th

Bur. J. Immunol. 17, 91-95, 1987

A:Title: Molecular analysis of the murine lupus-associated anti-self response: involvement

A:Reference number: S04573; MUID:87133856; PMID:3102255

A/Accession: S04576

A:Molecule type: mRNA

A:Residues: 1-136 <KOF>

A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030



C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 545.5; DB 2; Length 136;  
Best Local Similarity 88.9%; Pred. No. 1.2e-32;  
Matches 104; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLQSGAEIVSRGASVKISCTASGFINIKDYHWKVKRPEQGLEWIGIDPENGTLEY 60  
Db 20 EVQLQQSGAEIVSRGASVKISCTASGFINIKDYHWKVKRPEQGLEWIGIDPENGTLEY 79  
QY 61 APFQKATMTADTSSNTAVIQLSLASEPTAVYVCFD-ALDYGGCTTAVSS 116  
Db 80 ASFQKATMTADTSSNTAVIQLSLASEPTAVYVCFD-ALDYGGCTTAVSS 136

## RESULT 7

A:Accession: A55491  
A:Status: preliminary  
A:Molecule type: mouse  
A:Residues: 1-112 <GAP>

C:Species: Mus musculus (house mouse)  
C>Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 21-Jan-2000  
C/Accession: A55491  
R/Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.  
J. Biol. Chem. 269, 32389-32393, 1994  
A>Title: Molecular cloning of a proteolytic antibody light chain.  
A:Reference number: A55491; PMID:95096089; PMID:7798628

A:Cross-references: GB:L34775  
A:Note: authors translated the codon TAT for residue 37 as Thr  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 541; DB 2; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2e-32;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 191  
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 60  
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 243  
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 112

## RESULT 8

A:Accession: A36259  
A:Status: preliminary  
A:Molecule type: mouse  
A:Residues: 1-112 <ZILL>

C:Species: Mus musculus (house mouse)  
C>Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Jan-2000  
C/Accession: A36259  
R/Zilber, B.; Scherf, T.; Levitt, M.; Angilster, J.  
Biochemistry 29, 10032-10041, 1990  
A>Title: NMR-derived model for a peptide-antibody complex.  
A:Reference number: A36259; PMID:91104915; PMID:2271636  
A:Accession: A36259  
A:Status: preliminary  
A:Molecule type: mouse  
A:Residues: 1-112 <ZILL>  
A:Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 539; DB 2; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2.8e-32;  
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 191  
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 60  
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 243  
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 112

## RESULT 9

A:Accession: S20709  
A:Status: preliminary  
A:Molecule type: mouse  
A:Residues: 1-111 <SRE>

C:Species: Mus musculus (house mouse)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C/Accession: S20709  
R/Brennan, D.M.; Hands, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; O  
submitted to the EMBL Data Library, April 1992  
A>Description: Binding specificity and variable region sequences of two monoclonal ant  
A:Reference number: S20706  
A:Accession: S20709  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-111 <SRE>  
A:Cross-references: EMBL:Z11917; NID:952655; PIDN:CAA77975.1; PID:952656  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 537; DB 2; Length 111;  
Best Local Similarity 91.9%; Pred. No. 3.9e-32;  
Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 191  
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDSGKTYLWMLQRPQSPKRLIYVSKLD 60  
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 242  
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 111

## RESULT 10

A:Accession: S15672  
A:Status: preliminary  
A:Molecule type: mouse  
A:Residues: 1-116 <TEMA>

C:Species: Mus musculus (house mouse)  
C>Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S15672  
R/Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris  
Bio/Technology 9, 266-271, 1991  
A>Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial  
A:Reference number: S15672; PMID:9137412; PMID:1367535  
A:Accession: S15672  
A:Status: preliminary  
A:Molecule type: nucleic acid sequence not shown  
A:Residues: 1-116 <TEMA>  
A:Cross-references: EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 528; DB 2; Length 116;  
Best Local Similarity 84.3%; Pred. No. 1.8e-31;  
Matches 97; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 VOLQSGAEIVSRGASVKISCTASGFINIKDYHWKVKRPEQGLEWIGIDPENGTLEYA 61  
Db 2 VOLQSGAEIVSRGASVKISCTASGFINIKDYHWKVKRPEQGLEWIGIDPENGTLEYA 61  
QY 62 PKFQKATMTADTSSNTAVIQLSLASEPTAVYVCFD-ALDYGGCTTAVSS 116  
Db 62 PKFQKATMTADTSSNTAVIQLSLASEPTAVYVCFD-ALDYGGCTTAVSS 116



S31577

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C;Accession: S31577

R;Reclinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two anti-

A;Reference number: S31577

A;Accession: S31577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-131 <RBC>

A;Cross-references: EMBL:Z19575; NID:953983; PIDN:CA479627.1; PID:G53984

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 509; DB 2; Length 131;

Best Local Similarity 86.6%; Pred. No. 4.8e-30;

Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY	132	DVMTQPLTLSTIGOPASISCKSGSLDSDGKTYLWMLQPGQSPKRLTYIVSKLD	191
DB	20	DVMTQAPLTLSTIGOPASISCKSSHLISIDGKTYLWMLQPGQSPKRLTYIVSKLD	79
QY	192	SGVPRFRTSGSGSDFTLKINRYEADLGVYCMQGTSPFTFGAGTKLEIK	243
DB	80	SGVPRFRTSGSGSDFTLKINRYEADLGVYCMQGTSPFTFGAGTKLEIK	131

Search completed: July 30, 2004, 11:21:46  
Job time : 14.3354 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:15:41 ; Search time 7.90244 Seconds  
(without alignments)  
1601.157 Million cell updates/sec

Title: US-09-297-181-2  
Perfect score: 1289  
Sequence: 1 QVQLQSGAEIYRSGASVKL.....CMQGTSPITFGATYLEIK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	36.4	133	1	KV2F_HUMAN
2	428	33.2	113	1	KV2B_HUMAN
3	428	33.2	113	1	KV2D_HUMAN
4	428	33.2	113	1	KV2G_MOUSE
5	423	32.8	117	1	KV2E_HUMAN
6	423	32.8	139	1	HV07_MOUSE
7	418.5	32.5	115	1	KV2A_HUMAN
8	405.5	31.5	120	1	HV03_MOUSE
9	399	31.0	137	1	HV11_MOUSE
10	397.5	30.8	140	1	HV02_MOUSE
11	396.5	30.8	112	1	KV2C_HUMAN
12	384.5	29.8	117	1	HV12_MOUSE
13	384	29.8	147	1	HV1C_HUMAN
14	382	29.6	113	1	KV2C_MOUSE
15	382	29.6	113	1	KV2F_MOUSE
16	380.5	29.5	117	1	HV13_MOUSE
17	380	29.3	118	1	HV51_MOUSE
18	378	29.3	112	1	KV2A_MOUSE
19	377	29.2	113	1	KV2E_MOUSE
20	377	29.2	120	1	HV50_MOUSE
21	375.5	29.1	138	1	HV48_MOUSE
22	372.5	28.9	111	1	KV3N_MOUSE
23	372.5	28.9	116	1	HV15_MOUSE
24	371	28.8	112	1	KV2D_MOUSE
25	367.5	28.5	121	1	KV3M_MOUSE
26	367.5	28.5	121	1	HV01_MOUSE
27	365.5	28.4	108	1	KV1_MOUSE
28	365.5	28.4	111	1	KV1_CANPA
29	364	28.2	117	1	HV09_MOUSE
30	363.5	28.2	111	1	KV3L_MOUSE
31	360.5	28.0	111	1	KV3O_MOUSE
32	359	27.9	110	1	KV3P_MOUSE
33	358.5	27.8	134	1	KV4C_HUMAN

34	358	27.8	117	1	HV06_MOUSE
35	352	27.3	117	1	HV04_MOUSE
36	352	27.3	117	1	HV49_MOUSE
37	351	27.2	117	1	HV1B_HUMAN
38	350.5	27.2	111	1	KV3U_MOUSE
39	350.5	27.2	114	1	KV4A_HUMAN
40	349.5	27.1	111	1	KV3K_MOUSE
41	348.5	27.0	111	1	KV3S_MOUSE
42	348	27.0	117	1	HV1O_MOUSE
43	348	27.0	117	1	HV52_MOUSE
44	347.5	27.0	111	1	KV3H_MOUSE
45	345.5	26.8	131	1	KV3I_MOUSE

## ALIGNMENTS

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RESULT 1
KV2F_HUMAN
ID KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Kloback H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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DR EMBL; Z00020; CAAT7315.1; -.
DR PIR; A01890; K2HDP.
DR HSSP; P80362; IMTL.
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 133 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 133 BY SIMILARITY.
FT NON TER 133
SQ
SEQUENCE 133 AA; 14707 MW; 5130CAAC3673009EE CRC64;
Query Match 36.4%; Score 469; DB 1; Length 133;
Best Local Similarity 76.7%; Pred. No. 16-29;
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
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QY	128	GGGSDVMTGCPPLTSLTYIIGQPASISCKSSQSLSDSGKTYINMLQRPQSPKRLITLY	187
Db	17	GSSSDVMTGSPSLPVTLLGQPASISCKSSQSLVSDGNTLYINMFQGRFGQSPKRLITKY	76
QY	188	SKLDSGVPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPILTFGAGTKLEIK	243
Db	77	SNRDSGVPDRFSGSGSGTDFTLKISRVAEDVGVYYCMQGTHMSWTFGQTKVEIK	132
RESULT 2			
KV2B_HUMAN	ID	STANDARD;	PRT; 113 AA.
AC	P01615;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	IG kappa chain V-II region FR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=76253627; PubMed=821524;		
RA	Riesen W.F., Jaton J.-C.;		
RT	"Variable region sequence of the light chain from a Waldenstroms IgM		
RT	with specificity for phosphorylcholine.";		
RL	Biochemistry 15:13829-13833(1976).		
CC	-I- WISCCELLABOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S		
CC	MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.		
DR	PIR; A01886; K2HUF.		
DR	HSSP; P01607; IREI.		
DR	GO: GO:0005576; C:extracellular; NAS.		
DR	GO: GO:0003823; F:antigen binding; NAS.		
DR	GO: GO:0006955; P:immune response; NAS.		
DR	InterPro: IPR007110; IG-like.		
DR	InterPro: IPR003596; IG_V.		
DR	Pfam: PF00047; IG; 1.		
DR	SMART: SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG LIKE; 1.		
KM	Immunoglobulin V region.		
FT	DOMAIN	1	23
FT	DOMAIN	24	39
FT	DOMAIN	40	54
FT	DOMAIN	55	61
FT	DOMAIN	62	93
FT	DOMAIN	94	102
FT	DOMAIN	103	112
FT	DISULFID	23	93
FT	NON TER	113	113
SO	SEQUENCE	113 AA;	12660 MW; 0C0DA39E4EDB96BE CRC64;
Query Match 33.2%; Score 428; DB 1; Length 113;			
Best Local Similarity 71.4%; Pred. No. 1.3e-26;			
Matches 80; Conservative 14; Mismatches 18; Indels 0; Gaps 0			
QY	132	DVIMNQTPLTSLVTTGQPASISCKSSQSLSDSGKTYINMLQRPQSPKRLIYVSKLD	191
Db	1	DVIMNQTSPFLPVTLLGQPASISCKSSQSLVYHSGTYILBMYLQKQSGSEPLLIVSSYRD	60
QY	192	SGVDPDRFTGSGSGTDFTLKINRVAEDLGVYYCMQGTHSPILTFGAGTKLEIK	243
Db	61	SGVDPDRFSDSGSGTDFTLKIRVQEDVGVYYCMQATZSPYFGQTKLZIK	112
RESULT 3			
KV2D_HUMAN	ID	STANDARD;	PRT; 113 AA.
AC	P01617;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	

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DE Ig kappa chain V-II region TW.
OS Homo sapiens (Human) .
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEM) .
RA MEDLINE=74148480; PubMed=4596149;
RX Putnam F.W., Whitley E.J., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RL Primary amyloidosis." ;
RB Biochemistry 12:3763-3780(1973) .
RN [2]
RP SEQUENCE OF I-27 (AMYLOID PROTEIN TEM) .
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
RQ Glenner G.G.
RA "Glomerular identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973) .
CC -I MISCELLANEOUS : THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -I MISCELLANEOUS : THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSGRASIA AND AMYLOIDOSIS .
CC -I MISCELLANEOUS : THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR , A90370; KZHUW.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPRO07110; Ig-like.
DR InterPro; IPRO03596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IgV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT FT 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT FT 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT FT 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3G8F81FLI43CA CEC64;
Query Match 33.2%; Score 428; DB 1; Length 113;
Best Local Similarity 71.4%; Pred. No. 1,3e+26;
Matches 80; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
OY 132 DVLMQTGLTITSVLTIGDPASISCKSSQSLLDSCKTYNNMLLPKPGSPKRLIVYSKLDD 191
DB 1 DIVMTQSLSLTPVPPEPASISCKSSSOLLSDGDFDYNWLTKPKGQSFZZLIYALSNRA 60
OY 192 SGVDPRFGSGSGTDFTLKIRVAEADLGVVYCQGTHSPPLNFAAGTRLRIK 243
DB 61 SGVDPRFGSGSGTDFTLKIRVAEDDYGVYYCNMALQAPTFGGGTLEIK 112
RESULT 4
KV2G_MOUSE STANDARD; PR1; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-OCT-1986 (Rel. 01, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse) .
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

```

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RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RU Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KXMS26.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 FRAMEWORK-3.
FT DOMAIN 55 61 FRAMEWORK-4.
FT DOMAIN 62 93 FRAMEWORK-5.
FT DOMAIN 94 102 FRAMEWORK-6.
FT DOMAIN 103 112 FRAMEWORK-7.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 33.2%; Score 428; DB 1; Length 113;
Matches 83; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 132 DYVMQTPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYVSKD 191
DB 1 DYVMQTPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYVSKD 191

QY 192 SCVDPFRFGSSGSGDFTLKINRVEADLVGYVCMQGTSPLTFGAGTKLEIK 243
DB 61 SCVDPFRFGSSGSGDFTLKINRVEADLVGYVCMQGTSPLTFGAGTKLEIK 112

RESULT 5
KV2E_HUMAN STANDARD; PRT; 117 AA.
ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DC 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RU diversity.";
RU Nature 309:73-76(1984).
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CC EMBL; 200009; -; NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
CC HSSP; P80362; 1MTL.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL 1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 127 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E58B1 CRC64;

Query Match
Best Local Similarity 32.8%; Score 423; DB 1; Length 117;
Matches 81; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 128 GGSGDYVMQTPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYV 187
DB 1 GGSGDYVMQTPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYV 187

QY 188 SKLDGVPDRFRFGSSGSGDFTLKINRVEADLVGYVCMQGTSPLTFGAGTKLEIK 243
DB 61 SKLDGVPDRFRFGSSGSGDFTLKINRVEADLVGYVCMQGTSPLTFGAGTKLEIK 116

RESULT 6
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RU antibodies: somatic mutation evident in a gamma 2a variable region.";
RU Cell 24:635-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00529; AAA38170.1; -.
CC PIR; A90809; MEMS18.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.

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DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 124 D SEGMENT.  
 FT DOMAIN 125 139 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 139 139  
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;  
 Query Match 32.8%; Score 423; DB 1; Length 139;  
 Best Local Similarity 67.5%; Pred. No. 3.9e-26;  
 Matches 81; Conservative 15; Mismatches 20; Indels 4; Gaps 2;  
 QY 1 QVQLQSGAEIVRSGASVKLSCTASGPNIKDYIMHWKQRPPEGGLMIGIDENGDTX 60  
 DB 20 QVQLQSGAEIVRSGASVKLSCTASGPNIKDYIMHWKQRPPEGGLMIGIDENGDTX 79  
 QY 61 APFGGKATMTADSSNTAYLTSLASEDTAVYCC--NFYGA-LDYWGQGTIVYSS 116  
 DB 80 NEFKSKATLTVDKPSSTAYMQLSLTSEDAVYICARVYIGSSYVDYWGQGTITLVSS 139  
 RESULT 7  
 KW2A\_HUMAN STANDARD; PRT; 115 AA.  
 ID P01614;  
 AC P01614;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region Cum.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 OX [1]  
 RN RP  
 RP MEDLINE=68242259; PubMed=5586923;  
 RA Hilschmann N.;  
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
 RN [2]  
 RN REVISIONS TO 50: 52; 96 AND 97.  
 RX MEDLINE=70063440; PubMed=4188189;  
 RA Hilschmann N.;  
 RT "Molecular basis of antibody formation.";  
 RT Naturwissenschaften 56:195-205(1969).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC PIR; B91639; K2HUCM.  
 DR HSSP; P01607; IREI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-LIKE.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 KW DISULFID 24 95 BY SIMILARITY.  
 FT NON TER 115 115  
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F0A379569EC CRC64;

Query Match 32.5%; Score 418.5; DB 1; Length 115;  
 Best Local Similarity 72.6%; Pred. No. 7e-26; 17; Indels 1; Gaps 1;  
 Matches 82; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 QY 132 DVLMQPTLTSLVTTIGOPASISCKSSQSLDS-DKTYLNLMLQRPQSPKRLIYVSKL 190  
 DB 2 DIVMQLTSLPLFTVTEGPASISCKSSQSLDSQDNGTYLNLMLQKAGQSPQLIYTLVSK 61  
 QY 191 DSGVDRFTSGSSGDTFTIKINVEADLIGVYCCWQHTSPILFGAGTLEIK 243  
 DB 62 ASGVDRFSGSSGDTFTIKISRVQAEVGVYCCWQRIEIPYFGQIKLEIR 114  
 RESULT 8  
 KW03\_MOUSE STANDARD; PRT; 120 AA.  
 ID HV03\_MOUSE  
 AC P01747;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 OX [1]  
 RN RP  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8311846; PubMed=6186498;  
 RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate idiotype response of the strain A mouse.";  
 RT Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT. JH2.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-LIKE.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 KW DOMAIN 1 111 Ig-LIKE.  
 FT NON TER 120 120  
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;  
 Query Match 31.5%; Score 405.5; DB 1; Length 120;  
 Best Local Similarity 65.0%; Pred. No. 7.4e-25;  
 Matches 78; Conservative 18; Mismatches 19; Indels 5; Gaps 2;  
 QY 2 VOLQSGAEIVRSGASVKLSCTASGPNIKDYIMHWKQRPPEGGLMIGIDENGDTX 61  
 DB 1 VOLQSGAEIVRSGASVKLSCTASGPNIKDYIMHWKQRPPEGGLMIGIDENGDTX 60  
 QY 62 PKFGKATMTADSSNTAYLTSLASEDTAVYCC--NFYGA-LDYWGQGTIVYSS 116  
 DB 61 EKFGKATLTVDKPSSTAYMQLSLTSEDAVYICARVYIGSSYVDYWGQGTITLVSS 120  
 RESULT 9  
 KW11\_MOUSE STANDARD; PRT; 137 AA.  
 ID HV11\_MOUSE  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 843 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botchwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RT Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MENA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; J00539; AAA8172.1; -.
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; AD5881BF44B8E09 CRC64;

Query Match 31.0%; Score 399; DB 1; Length 137;
Best Local Similarity 66.1%; Pred. No. 2.7e-24;
Matches 78; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 60
DB 20 QVQLQSGAEIVSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 79
QY 61 APEFGKATMTADTSNTAYLQLSASEDTAYYCNFY--GPAIDYWGCGTIVYSS 116
DB 80 NEHFKKATLTIDKBSSTAYMQLSLTSEDSAVYYCARIRLGRFYDWGGTTLTVSS 137

RESULT 10
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;

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RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; J00493; AAA8128.1; -.
DR PIR; A94264; HWMSG7.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 30.8%; Score 397.5; DB 1; Length 140;
Best Local Similarity 62.8%; Pred. No. 3.7e-24;
Matches 76; Conservative 19; Mismatches 21; Indels 5; Gaps 2;

QY 1 QVQLQSGAEIVSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 60
DB 20 QVQLQSGAEIVSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 79
QY 61 APEFGKATMTADTSNTAYLQLSASEDTAYYCNFY--NFYSDA--LDYWGCGTIVYSS 115
DB 80 NEHFKKATLTIDKBSSTAYMQLSLTSEDSAVYYCARSHYYGSGYDFYWGCGTTLTVS 139
QY 116 S 116
DB 140 S 140

RESULT 11
KV2C HUMAN STANDARD; PRT; 112 AA.
ID KV2C HUMAN
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-OUT-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSSP; P80362; 1WTU.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE, PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 102 111 FRAMEWORK-4.  
 FT NON\_TER 112 112 BY SIMILARITY.  
 SQ SEQUENCE 112 AA; 12055 MW; E5B2E2FA7ABE481 CRC64;  
 Query Match 30.8%; Score 396.5; DB 1; Length 112;  
 Best Local Similarity 63.4%; Pred. No. 3.4e-24;  
 Matches 71; Conservative 25; Mismatches 15; Indels 1; Gaps 1;  
 QY 132 DVMTQTEPLTSLVITIGQPASISCKSSQSLSDSGKTYLNLORPGSPKRLIYVSKLD 191  
 DB 1 DIVLTQSPSLPYTPGPPASISCKSSQNLISBGB-YLDWYTLKPGGSPZLLIILYLSNRA 59  
 QY 192 SGVEDRFTSGSGGTDFTLKINRYEADIGVYVCMQGHSPLTFGAGTKLEIK 243  
 DB 60 SGVFNRRSSGSGGTBFLTKISRVZABVGYVCMQALQTEPLTFGSGTNVEIK 111  
 RESULT 12  
 HV12 MOUSE STANDARD; PRT; 117 AA.  
 ID HV12 MOUSE  
 AC P01756;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 104E.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.  
 RX MEDLINE=81075344; PubMed=6816276;  
 RA Kehry M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
 RA Hood L.E.,  
 RT "Complete amino acid sequence of a mouse mu chain: homology among  
 RT heavy chain constant region domains.";  
 RL Biochemistry 21:5415-5424(1982).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR; A02039; MHMS4E.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 FT DOMAIN 1 116 IG-LIKE.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT CARBOHD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACB4BE447E41 CRC64;  
 Query Match 29.8%; Score 384.5; DB 1; Length 117;  
 Best Local Similarity 65.0%; Pred. No. 3e-23;  
 Matches 76; Conservative 12; Mismatches 28; Indels 1; Gaps 1;  
 QY 1 QVQLQDSGAELVRSASVYKLSCTASGFINIKYIMHWVYKORPEQGLFWIGIDPENGDTEY 60  
 DB 1 EVQLQDSGPELVKPGASVYMSCKASGYFTFDYIMRWVYKSHKSLDIEMINPNNGTISY 60  
 QY 61 APEFGKATMTADTSSNTAYVQLSSLASDPAVYVC-NFYGDALDYWGQTTVTYVSS 116

DB 61 NQKFKKATLTVDKSSSTAYMQNLNLTSDSAVYYCARDWYFDWYGAGTIVTVSS 117  
 RESULT 13  
 HV1C HUMAN STANDARD; PRT; 147 AA.  
 ID HV1C HUMAN  
 AC P01744;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region ND precursor (Fragments).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83065234; PubMed=6815656;  
 RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
 RA Bell L.O., Gould H.J.;  
 RT "Cloning and sequence determination of the gene for the human  
 RT immunoglobulin epsilon chain expressed in a myeloma cell line.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
 RN [2]  
 RP SEQUENCE OF 20-147.  
 RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
 RL (In) Bach M.K. (eds.);  
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
 RL Marcel Dekker, New York (1978).  
 CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC HSSP; P01789; IMCP.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.  
 KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.  
 FT SIGNAL 1 19  
 FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.  
 FT DOMAIN 20 131 IG-LIKE.  
 FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 41 115 T -> V (IN REF. 2).  
 FT CONFLICT 21 21 IH -> HI (IN REF. 2).  
 FT CONFLICT 53 54 VG -> GV (IN REF. 2).  
 FT CONFLICT 67 68 MISSING (IN REF. 2).  
 FT NON\_TER 125 125  
 FT NON\_TER 147 147  
 SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A536C20 CRC64;  
 Query Match 29.8%; Score 384; DB 1; Length 147;  
 Best Local Similarity 56.2%; Pred. No. 4.3e-23;  
 Matches 72; Conservative 18; Mismatches 26; Indels 12; Gaps 2;  
 QY 1 QVQLQDSGAELVRSASVYKLSCTASGFINIKYIMHWVYKORPEQGLFWIGIDPENGDTEY 60  
 DB 20 QTVLVQSGAEVRSASVYKLSCTASGFINIKYIMHWVYKORPEQGLFWIGIDPENGDTEY 79  
 QY 61 APEFGKATMTADTSSNTAYVQLSSLASDPAVYVC-NFYGDALDYWGQTTVTYVSS 108  
 DB 80 APEFGKATMTADTSSNTAYVQLSSLASDPAVYVC-NFYGDALDYWGQTTVTYVSS 139  
 QY 109 GTTVTVSS 116  
 DB 140 GTTVTVSS 147  
 RESULT 14  
 KV2C\_MOUSE

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ID      KV2C MOUSE      STANDARD;      PRT;      113 AA.
AC      P01628;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region MOPC 511.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=81052016; PubMed=6776396;
RA      Appella E.;
RT      Amino acid sequence of the light chain variable region of M511, a
RL      Mol. Immunol. 17:711-718 (1980).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC      BINDS PHOSPHORYLCHOLINE.
DR      PIR; A01910; KWMS1.
DR      HSSP; P80362; IWTU.
DR      InterPro; IPR007110; Ig_1Ike.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; Ig_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 40 54 FRAMEWORK-2.
FT      DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 62 93 FRAMEWORK-3.
FT      DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 103 112 FRAMEWORK-4.
FT      DISULFID 23 93 BY SIMILARITY.
FT      NON TER 113 113
SQ      SEQUENCE 113 AA; 12496 MW; EFBDQ4DA2BD3450 CRC64;

Query Match 29.6%; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 4.5e-23;
Matches 75; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY      132 DVLMTQPTLSTVIGQSPASISCKSSQSLDSDGKTYINWLLQRPQSPKRLIYVSKLD 191
DB      1 DIVITQDELSTKPTSGSESVISCRSSKSLIYKDKTYINWFLQGPQSPRLIYIMSTRA 60

QY      192 SGVPPRFSGSGGTFTLKINRVEADLVGYVYCMQGTHSPLTPFGAGTKLEIK 243
DB      61 SGVSPRFSGSGGTFTLKINRVEADLVGYVYCMQGTHSPLTPFGAGTKLEIK 112

RESULT 15
KV2F MOUSE
ID      KV2F MOUSE      STANDARD;      PRT;      113 AA.
AC      P01630;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region 7S34.1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=83256427; PubMed=6409088;
RA      Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT      A new isotype sequence (V kappa 27) of the variable region of kappa-
RT      light chains from a mouse hybridoma-derived anti-(streptococcal group
RT      A polysaccharide) antibody containing an additional cysteine residue.
RT      Application of the dimethylaminoozobenzene isothiocyanate technique
RT      for the isolation of peptides.";
RL      Biochem. J. 211:173-180 (1983).

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CC      -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC      ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR      PIR; A01913; KWMS7S.
DR      HSSP; P80362; IWTU.
DR      InterPro; IPR007110; Ig_1Ike.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; Ig_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 40 54 FRAMEWORK-2.
FT      DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 62 93 FRAMEWORK-3.
FT      DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 103 112 FRAMEWORK-4.
FT      DISULFID 23 93 BY SIMILARITY.
FT      NON TER 113 113
SQ      SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 29.6%; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 4.5e-23;
Matches 75; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY      132 DVLMTQPTLSTVIGQSPASISCKSSQSLDSDGKTYINWLLQRPQSPKRLIYVSKLD 191
DB      1 DIVITQDAPSLVTPESVSISCRSSKSLHSNGNTLYLWFLQRPQCCQLIYMSNLA 60

QY      192 SGVPPRFSGSGGTFTLKINRVEADLVGYVYCMQGTHSPLTPFGAGTKLEIK 243
DB      61 SGVPPRFSGSGGTFTLKINRVEADLVGYVYCMQGREYPTYPFGGATKLEIK 112

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Search completed: July 30, 2004, 11:19:46  
 Job time : 7.90244 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:06 ; Search time 34.5732 Seconds  
(without alignments)  
2217.642 Million cell updates/sec

Title: US-09-297-181-2  
Perfect score: 1289  
Sequence: 1 QVQLQSGAEIVRSAGSVKL.....CMQGTSPLTFGATKLEIK 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SP archaea:\*
  - 2: SP bacteria:\*
  - 3: SP fungi:\*
  - 4: SP human:\*
  - 5: SP invertebrate:\*
  - 6: SP mammal:\*
  - 7: SP mhc:\*
  - 8: SP organelle:\*
  - 9: SP phage:\*
  - 10: SP plant:\*
  - 11: SP rodent:\*
  - 12: SP virus:\*
  - 13: SP vertebrate:\*
  - 14: SP unclassified:\*
  - 15: SP rivirus:\*
  - 16: SP bacteriap:\*
  - 17: SP archaep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query	% Match	length	DB ID	Description
1	734	56.9	243	11	Q7TOM2	Q7TOM2 mus musculus
2	696.5	54.0	298	11	Q9GYFO	Q9GYFO mus musculus
3	657	51.0	241	11	Q921A6	Q921A6 mus musculus
4	620.5	48.1	218	11	Q925S1	Q925S1 mus musculus
5	522.5	40.5	468	11	Q991J1	Q991J1 mus musculus
6	511	39.6	148	11	Q8K122	Q8K122 mus musculus
7	497	38.6	239	11	Q8K0F8	Q8K0F8 mus musculus
8	472	36.6	239	4	Q8TCD0	Q8TCD0 homo sapien
9	450.5	34.9	170	11	Q925S2	Q925S2 mus musculus
10	448	34.8	238	11	Q99M37	Q99M37 mus musculus
11	448	34.8	239	11	Q8VC55	Q8VC55 mus musculus
12	447.5	34.7	114	4	Q9UL80	Q9UL80 homo sapien
13	443.5	34.4	109	11	Q918A5	Q918A5 mus musculus
14	438	34.0	238	11	Q8YCT6	Q8YCT6 mus musculus
15	435	33.7	143	11	Q924P9	Q924P9 mus musculus
16	432	33.5	239	4	Q8NEK0	Q8NEK0 homo sapien

17	428	33.2	118	11	Q921C4	Q921C4 mus musculus
18	428	33.2	482	11	Q8K172	Q8K172 mus musculus
19	426.5	33.1	146	11	Q924R8	Q924R8 mus musculus
20	425.5	33.0	142	11	Q924Q1	Q924Q1 mus musculus
21	423.5	32.9	146	11	Q924Q3	Q924Q3 mus musculus
22	423	32.8	145	11	Q924Q7	Q924Q7 mus musculus
23	422	32.7	145	11	Q924P7	Q924P7 mus musculus
24	422	32.7	145	11	Q924R1	Q924R1 mus musculus
25	419	32.5	143	11	Q924R0	Q924R0 mus musculus
26	419	32.5	145	11	Q924Q6	Q924Q6 mus musculus
27	418	32.4	145	11	Q924Q9	Q924Q9 mus musculus
28	418	32.4	145	11	Q924R4	Q924R4 mus musculus
29	415	32.2	473	11	Q99125	Q99125 mus musculus
30	414.5	32.2	144	11	Q924P5	Q924P5 mus musculus
31	412.5	32.0	481	11	Q91WT1	Q91WT1 mus musculus
32	412	32.0	137	11	Q924R6	Q924R6 mus musculus
33	412	32.0	143	11	Q91V67	Q91V67 mus musculus
34	411.5	31.9	140	11	Q924R2	Q924R2 mus musculus
35	409.5	31.8	142	11	Q924Q2	Q924Q2 mus musculus
36	409	31.7	143	11	Q924R7	Q924R7 mus musculus
37	409	31.7	473	11	Q9D8L4	Q9D8L4 mus musculus
38	407	31.6	143	11	Q924Q5	Q924Q5 mus musculus
39	407	31.6	488	11	Q8K0F2	Q8K0F2 mus musculus
40	405	31.4	145	11	Q924R3	Q924R3 mus musculus
41	404.5	31.4	140	11	Q924P8	Q924P8 mus musculus
42	404	31.3	139	11	Q924R5	Q924R5 mus musculus
43	404	31.3	141	11	Q924Q4	Q924Q4 mus musculus
44	404	31.3	143	11	Q91VA2	Q91VA2 mus musculus
45	404	31.3	143	11	Q924P6	Q924P6 mus musculus

ALIGNMENTS

RESULT 1

ID	Q7TOM2	PRELIMINARY;	PRT;	243 AA.
AC	Q7TOM2;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	SCFV 6H8 protein (Fragment).			
GN	SCFV 6H8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAT=Balb/C;			
RA	Peter J.C., Eftekhari P., Billiard P., Wallukat G.,			
RT	"scfv single chain antibody variable region agonist for			
RT	the beta-2 adrenergic receptor."			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ574851; CAE00495.1; -			
FT	NON TER			
SO	SEQUENCE	243 AA;	25976 MW;	BHFF64D2DCFA76 CRC64;
Query Match				
Best local Similarity 56.9%; Score 734; DB 11; Length 243;				
Matches 145; Conservative 32; Mismatches 60; Indels 6; Gaps 2;				
QY	1 QVQLQSGAEIVRSAGSVKLSTCTAGSFGFNKDYIMHWVKRPRQGLFWIGMIDPNDLEY 60			
DB	1 QVQLQSGAEIVRSAGSVKLSTCTAGSFGFNKDYIMHWVKRPRQGLFWIGMIDPNDLEY 60			
QY	61 AKRFGKATMTADTSSTAYVLCSTLASDETVAYVYCNFGDALDYWGQGTTVTSGGGG 120			
DB	61 DEKFKKGLITDPTSSSTAYVLCSTLASDETVAYVYCNFGDALDYWGQGTTVTSGGGG 120			
QY	121 SGGGSGGGGSGVLMTCPTLTLSVTIGQPAISCKSSGSLDSDGKTYINMLIQPGGP 180			
DB	121 SGGGSGGGGSGVLMTCPTLTLSVTIGQPAISCKSSGSLDSDGKTYINMLIQPGGP 180			



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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cai D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER
SQ SEQUENCE 218 AA; 23013 MW; 5274FA8F7982817 CRC64;

Query Match 48.1%; Score 620.5; DB 11; Length 218;
Best Local Similarity 53.9%; Pred. No. 1,5e-43;
Matches 117; Conservative 44; Mismatches 53; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVSGASVKSCTASGFINIKDYVHWKORPFGQLEWIGIDPENGDTEY 60
DQ 3 QVQLQSGPELKKRGKTVRSCKASGVTFTTAGMOWKMPGKLGKMWIGINTHSGVPKY 62
QY 61 APKFGKATMTADTSNTAVYLQLSLASEDTAVYYCN--FYGDALDYWGQGTIVTVSSG 118
DQ 63 APKFGKRFAPSLSTASAVYLQISLNKNEDTATYFCMRNDYDGFAYWGQGTIVTVSSG 122
QY 119 GSGGGSGSGGSDVMTQTPELTSLTIGIPASICKSSQLSDSGKTYIMKLQRPQ 178
DQ 123 GSGGGSGSGGSDIVLTQSPASLAVSLGGRATISGRASS--VDNIGISPMFWQKPPQ 181
QY 179 SPKRLIYIVSKLDSGVPDRFTSGSGTDFTLKINRYE 215
DQ 182 PKKLIYVASKSGSGVPAGLLASGSDTDSINITYWE 218

RESULT 5
QY 099L31 PRELIMINARY; PRT; 468 AA.
ID 099L31;
AC 099L31;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR PDB; 2A22; 24-NOV-99.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 40.5%; Score 522.5; DB 11; Length 468;
Best Local Similarity 83.2%; Pred. No. 5,2e-35;
Matches 99; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQSGAEIVSGASVKSCTASGFINIKDYVHWKORPFGQLEWIGIDPENGDTEY 60
DQ 20 EVQLQSGAEIVRPGASVSLCTASGFINIKDSLMMHWKORPFGQLEWIGIDPENGDTEY 79
QY 61 APKFGKATMTADTSNTAVYLQLSLASEDTAVYYCN--FYGDALDYWGQGTIVTVSS 116

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DQ 80 APKFGKATMTADTSNTAVYLQLSLASEDTAVYYCARNLLYGGYDYWGQGTIVTVSS 138

RESULT 6
QY 08K122 PRELIMINARY; PRT; 148 AA.
ID 08K122;
AC 08K122;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028925; AAH28925.1; -.
DR InterPro; IPR003599; IGV.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 39.6%; Score 511; DB 11; Length 148;
Best Local Similarity 97.0%; Pred. No. 1,1e-34;
Matches 97; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 132 DVMTQTPELTSLTIGIPASICKSSQLSDSGKTYIMKLQRPQSPKRLIYIVSKLD 191
DQ 20 DVMTQTPELTSLTIGIPASICKSSQLSDSGKTYIMKLQRPQSPKRLIYIVSKLD 79
QY 192 GSVDPDRFTSGSGTDFTLKINRYEADLGVYVQWQGTSP 231
DQ 80 GSVDPDRFTSGSGTDFTLKINRYEADLGVYVQWQGTSP 119

RESULT 7
QY 08K0F8 PRELIMINARY; PRT; 239 AA.
ID 08K0F8;
AC 08K0F8;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IGV.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.

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ID	Q8VC55	PRELIMINARY;	PRT;	239 AA.
AC	Q8VC55;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1] _			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC021781; AAH21781.1; _			
DR	PIR; A33933; A33933.			
DR	PDB; 1KCS; 24-JUL-02.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0015070; F:toxin activity; IEA.			
DR	GO; GO:0009405; F:pathogenesis; IEA.			
DR	InterPro; IPR004214; Conotoxin.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF02950; Conotoxin; 1.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00406; IgV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; 1.			
DR	Hypothetical protein_			
DR	SEQUENCE 239 AA; 26303 MW; C161190CA25C337 CRC64;			

RESULT 13	
Q9JL85	
ID	Q9JL85
AC	Q9JL85;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Anti-Amyosin immunoglobulin heavy chain variable region (Fragment).
DD	
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Maltin S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 34.4%; Score 443.5; DB 11; Length 109;
Best Local Similarity 78.9%; Pred. No. 2.8e-29;
Matches 86; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 9 AELVRSGAVKLSCTASGFNIKDYMHVWVQKPEQGLEWIGMIDPENGDTEYAPKQGKA 68
Db 1 AELVKGASVYKLSCTASGFNIEDTYMHVWVQKPEQGLEWIGRIDPAHGSHKYPKFGKA 60

RESULT 14
QY 69 TMTADTSSNTAYQLSLASEDTAVYYCNFYGDAL-DYMGQGTIVYSS 116
Db 61 TITSSTSSNTAYQLSLTSEDYAVYYCVRGAVFDMGQGTALIVSS 109

ID Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Straube R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.
DR PIR; A32248; A32248.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.

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DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35BC08B3DE5414AD CRC64;

Query Match 34.0%; Score 438; DB 11; Length 238;
Best Local Similarity 75.2%; Pred. No. 2.2e-28;
Matches 85; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 131 SVYLMQTLELTSTYTGQFASISCKSSQSILSDGKTYNMLHPRGQSPKRLIYVSKL 190
Db 19 SDVVMQTPLSPVSGDQASISCKSSQSLVHNSNTYIHWYQKQGQSPKRLIYVSNR 78

QY 191 DSGVPRFTGSGSGTDFTLKINRVEAEDLVGYVYCWGTHSPITFGATKLEIK 243
Db 79 FSGVPRFSGSGSGTDFTLKISVEAEDLVGYVYCSQSTHVPFPGGTGLEIK 131

RESULT 15
QY 0924P9 PRELIMINARY; PRT; 143 AA.
ID 0924P9;
AC 0924P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
DN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
DR PIR; PH1161; PH1161.
DR PIR; PH1162; PH1162.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134FE CRC64;

Query Match 33.7%; Score 435; DB 11; Length 143;
Best Local Similarity 70.3%; Pred. No. 2e-28;
Matches 83; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVRSGAVKLSCTASGFNIKDYMHVWVQKPEQGLEWIGMIDPENGDTEY 60
Db 1 QVQLQGLAEIVKPGASVYKLSCTASGFNIEDTYMHVWVQKPEQGLEWIGMIDPSDYNY 60

QY 61 APKQGKATMTADTSSNTAYQLSLASEDTAVYYC-NFYGDADYMGQGTIVYSS 116
Db 61 TITSSTSSNTAYQLSLTSEDYAVYYCVRGAVFDMGQGTALIVSS 109

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Db 61 NQKFKKATLTVDTSSTAYMQLSLTSEDDSAVYCYASHYGGSSDYWGQGTTLTVSS 118

Search completed: July 30, 2004, 11:21:08  
Job time : 35.5732 secs

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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:14:51 ; Search time 49.0915 Seconds  
(without alignments)  
1433.128 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315  
Sequence: 1 QVRLQSGAEIVRSGASVNI.....YCKQSYNLPFGGKLEIK 249

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_297an04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003ps.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	100.0	249	2	AAW60770
2	1024.5	77.9	288	2	AAW82743
3	1024.5	77.9	673	2	AAW82742
4	961	73.1	243	2	AAW60769
5	955	72.6	535	2	AAW28491
6	955	72.6	535	2	AAW28492
7	951	72.3	580	2	AAW90217
8	942	71.6	556	2	AAW90218
9	932.5	70.9	437	2	AAW37738
10	931	70.8	258	5	AAU72865
11	930	70.7	248	2	AAU17960
12	924.5	70.3	240	6	ABJ26742
13	923.5	70.2	242	4	ABJ31422
14	921	70.0	248	2	AAV17964
15	917.5	69.8	238	5	AAE25963
16	917.5	69.8	238	5	AAU74420
17	917.5	69.8	238	5	AAU74420
18	913.5	69.5	240	5	AAE25960
19	913.5	69.5	240	5	AAU74419
20	913.5	69.5	240	6	ABJ26731
21	906	68.9	262	4	AAW31421
22	906	68.9	281	2	AAW82744
23	906	68.9	238	5	AAE25961
24	905.5	68.9	238	5	AAE25961
25	904	68.7	241	7	ADD31766

26	901	68.5	248	2	AAV17965	AAV17965	Mouse scf
27	899	68.4	240	7	ADD31766	ADD31766	Anti-CEA
28	897	68.2	271	4	AAW31423	AAW31423	Protein u
29	896.5	68.2	272	4	AAW31424	AAW31424	Protein u
30	891	67.8	500	7	ADD13792	ADD13792	Plasmid p
31	889.5	67.6	258	5	ABW05994	ABW05994	Mouse and
32	883.5	67.2	258	5	ABW05992	ABW05992	Monoclonal
33	883.5	67.2	258	5	ABW05990	ABW05990	Mouse mon
34	883.5	67.2	258	5	ABW05982	ABW05982	Monoclonal
35	883	67.1	270	2	AAU78719	AAU78719	MFE-23 an
36	882.5	67.1	258	5	AAU72871	AAU72871	3B10xP4-3
37	882.5	67.1	505	5	AAU72875	AAU72875	Human NK6
38	880	66.9	258	2	AAW90222	AAW90222	Anti-B7.2
39	879.5	66.9	444	6	ABJ39018	ABJ39018	CC49 sing
40	879	66.8	556	4	AAU80040	AAU80040	scFv-rear
41	879	66.8	556	4	AAU97935	AAU97935	scFv-rear
42	877.5	66.7	282	2	AAW09818	AAW09818	VH4715-1i
43	877.5	66.7	282	2	AAW35564	AAW35564	Anti-HIT-E
44	877	66.7	553	2	AAW11508	AAW11508	Single ch
45	877	66.7	553	2	AAW73223	AAW73223	H22-anti-

## ALIGNMENTS

RESULT 1  
ID AAW60770 standard; protein; 249 AA.  
XX  
AC AAW60770;  
XX  
DT 08-SEP-1998 (first entry)  
DE Single chain antibody (scFv) D3M that binds to mutant p53 proteins.  
XX  
XX Single chain antibody; scFv D3M; mouse; p53 protein; oligomerisation.  
KW regulatory domain; p53 mutant; H273; W248; G281.  
KW p53-dependent trans-activating activity; restoration;  
KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;  
KW cancer; re-stenosis; ss.  
XX  
XX Mus sp.  
OS  
PN WO9818825-A1.  
XX  
XX 07-MAY-1998.  
PD  
XX  
XX 27-OCT-1997; 97WO-FR001921.  
PF  
XX  
XX 29-OCT-1996; 96FR-00013176.  
PR  
XX  
XX (RHON ) RHONE-POULENC RORER SA.  
PA Bracco L, Debussche L;  
PI WPI 1998-272140/24.  
PI WPI 1998-272140/24.  
DR N-PSDB; AAV36237.  
XX  
XX Restoring p53-dependent trans-activating activity to cell containing  
PT mutant p53 - by delivering single-chain antibody specific for the mutant,  
PT particularly for treatment of tumours.  
XX  
XX Claim 5; Page 32; 54pp; French.  
XX  
XX The present sequence represents a single chain antibody (scFv) designated  
CC D3M. The antibody binds to an epitope present in the C-terminal region of  
CC the p53 protein that includes oligomerisation and regulatory domains,  
CC specifically between positions 320 and 393. scFv D3M is directed against  
CC p53 mutants, particularly H273, W248 and G281 mutants. When the scFv is  
CC introduced into cells containing a mutant p53 protein, p53-dependent  
CC trans-activating activity is restored. scFv D3M is specific for p53-  
CC mutants that have lost tumour-suppressing activity and are present in  
CC tumour cells. It is particularly used to treat hyper-proliferation

CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53

XX Sequence 249 AA;

Query Match 100.0%; Score 1315; DB 2; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-87;  
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSSGAEIVRSGASVNLSCIASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60  
 DB 1 QVQLQSSGAEIVRSGASVNLSCIASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60  
 QY 61 APNFGQKATVTADTSNTAVLHLSLTSEPTVYYCNNAVITYEYDGYALDYWGQGTITVY 120  
 DB 61 APNFGQKATVTADTSNTAVLHLSLTSEPTVYYCNNAVITYEYDGYALDYWGQGTITVY 120  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 180  
 DB 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 180  
 QY 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITSSVQAEADLAIVYCKOSYNIPTF 240  
 DB 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITSSVQAEADLAIVYCKOSYNIPTF 240  
 QY 241 GGGTKLEIK 249  
 DB 241 GGGTKLEIK 249

# RESULT 2

AAW82743 standard; protein; 288 AA.

XX ID AAW82743 standard; protein; 288 AA.  
 AC AAW82743;  
 DT 10-MAY-1999 (first entry)  
 XX DE Fusion protein PNG4/55.lscFv/CPG2 R6/del EcorI.  
 XX KM Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;  
 KM prodrug-converting enzyme; cell surface antigen; treatment; cancer;  
 KM inflammation; rheumatoid arthritis; antibody; prodrug therapy system.  
 XX OS Synthetic.  
 XX PN WO9851787-A2.  
 XX PD 19-NOV-1998.  
 XX PF 05-MAY-1998; 98WO-GB001294.  
 XX PR 10-MAY-1997; 97GB-00009421.  
 XX PA (ZENNE ) ZENECA LTD.  
 XX PI Emery SC, Blakey DC;  
 XX DR WPI, 1999-059700/05.  
 XX DR N-PSDB; AAV72064.  
 XX PT New gene construct expressing conjugate of targeting agent and prodrug-  
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.  
 XX PS Example 15; Page 82; 100pp; English.

CC This sequence is a used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-  
 CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target

CC site, then administration of (III) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system

XX Sequence 288 AA;

Query Match 77.9%; Score 1024.5; DB 2; Length 288;  
 Best Local Similarity 77.9%; Pred. No. 1.9e-66;  
 Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 QVQLQSSGAEIVRSGASVNLSCIASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60  
 DB 23 QVQLQSSGAEIVRSGASVNLSCIASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 82  
 QY 61 APNFGQKATVTADTSNTAVLHLSLTSEPTVYYCNNAVITYEYDGYALDYWGQGTITVY 120  
 DB 61 APNFGQKATVTADTSNTAVLHLSLTSEPTVYYCNNAVITYEYDGYALDYWGQGTITVY 120  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 180  
 DB 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 180  
 QY 142 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 201  
 DB 142 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVAMCKSSQSLFNSRTRKNYLAWYQ 201  
 QY 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITSSVQAEADLAIVYCKOSYNIPTF 240  
 DB 202 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITSSVQAEADLAIVYCKOSYNIPTF 261  
 QY 241 GGGTKLEIK 249  
 DB 262 GGGTKLEIK 270

# RESULT 3

AAW82742 standard; protein; 673 AA.

XX ID AAW82742 standard; protein; 673 AA.  
 AC AAW82742;  
 DT 10-MAY-1999 (first entry)  
 XX DE Plasmid PNG4/55.lscFv/CPG2 R6 protein.  
 XX KM Conjugate; cell targeting; cytotoxic drug; prodrug-converting enzyme;  
 KM cell surface antigen; treatment; cancer; inflammation; antibody;  
 KM rheumatoid arthritis; prodrug therapy system.  
 XX OS Synthetic.  
 XX PN WO9851787-A2.  
 XX PD 19-NOV-1998.  
 XX PF 05-MAY-1998; 98WO-GB001294.  
 XX PR 10-MAY-1997; 97GB-00009421.  
 XX PA (ZENNE ) ZENECA LTD.  
 XX PI Emery SC, Blakey DC;  
 XX DR WPI, 1999-059700/05.  
 XX DR N-PSDB; AAV72059.  
 XX PT New gene construct expressing conjugate of targeting agent and prodrug-  
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic  
 PT drug in vivo, especially for treatment of cancer.

XX Example 14; Page 78-79; 100pp; English.

CC This sequence is used in a method for obtaining a novel gene construct  
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-

CC targeting group (I) and a heterologous prodrug-converting enzyme (II),  
 CC and (B) is directed to leave the cell for selective localisation at a  
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target  
 CC site, then administration of (II) is used for targeted release of  
 CC cytotoxic drug, specifically for treating cancer but also inflammation  
 CC such as rheumatoid arthritis. In situ generation of the targeting  
 CC antibody increases selectivity, reducing side effects at normal tissue.  
 CC The method is applicable to any antibody-directed enzyme prodrug therapy  
 CC system  
 XX  
 SQ Sequence 673 AA;  
 Query Match 77.9%; Score 1024.5; DB 2; Length 673;  
 Best Local Similarity 77.9%; Pred. No. 4.3e-66;  
 Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 QVKLOESGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEX 60  
 Db 20 QVLOQSGAEIVNSGASVQLSCRASGTFYGMHWKORPGGLEWIGVNPSTGRSDY 79  
 QY 61 APNFOGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTTVV 120  
 Db 80 NEFEKXKATLVTKSSTTAYMQSLTSEDSAVYYCARERAYGD-AMDYWGQGTTVV 138  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLASAGKVMCKSSQSLFNSRTKNYLAWQ 180  
 Db 139 SSGGGSGGGSGGGSDIELSQSPSLASAGKVMCKSSQSLNSRTRKNYLAWQ 198  
 QY 181 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKQSYNLPTF 240  
 Db 199 QKPGSPKVLIVASTRTSGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKQSYNLPTF 258  
 QY 241 GGGTKLEIK 249  
 Db 259 GGGTKLEIK 267  
 RESULT 4  
 AAM60769  
 ID AAM60769 standard; protein; 243 AA.  
 AC AAM60769;  
 XX  
 DT 08-SEP-1998 (first entry)  
 DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.  
 XX  
 KW Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;  
 KW regulatory domain; p53 mutant; H273; W248; G281;  
 KW p53-dependent trans-activating activity; restoration;  
 KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;  
 KW cancer; re-stenosis; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9818825-A1.  
 PD 07-MAY-1998.  
 XX  
 PF 27-OCT-1997; 97WO-FR001921.  
 XX  
 PR 29-OCT-1996; 96FR-00013176.  
 XX  
 PA (RHON ) RHONE-POULENC RORER SA.  
 XX  
 PI Bracco L, Debussche L;  
 XX  
 DR WPT, 1998-272140/24.  
 DR N-PSDB; AAV36236.  
 XX  
 PT Restoring p53-dependent trans-activating activity to cell containing  
 PT mutant p53 - by delivering single-chain antibody specific for the mutant,  
 PT particularly for treatment of tumours.

XX  
 PS Claim 5; Page 31; 54pp; French.  
 XX  
 CC The present sequence represents a single chain antibody (ScFv) designated  
 CC 421. The antibody binds to an epitope present in the C-terminal region of  
 CC the p53 protein that includes oligomerisation and regulatory domains;  
 CC specifically between positions 320 and 393. ScFv 421 is directed against  
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is  
 CC introduced into cells containing a mutant p53 protein, p53-dependent  
 CC trans-activating activity is restored. ScFv 421 is specific for p53-  
 CC mutants that have lost tumour-suppressing activity and are present in  
 CC tumour cells. It is particularly used to treat hyper-proliferation  
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also  
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant  
 CC and to purify or detect p53  
 XX  
 SQ Sequence 243 AA;  
 Query Match 73.1%; Score 961; DB 2; Length 243;  
 Best Local Similarity 74.8%; Pred. No. 6.4e-62;  
 Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;  
 QY 1 QVKLOESGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEX 60  
 Db 1 QVLOQSGAEIVNSGASVXLSTASGFNPKDYMHVWKORPGGLEWIGMIDPENDTXY 60  
 QY 61 APNFOGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTTVV 120  
 Db 61 APNFOGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTTVV 114  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLASAGKVMCKSSQSLFNSRTKNYLAWQ 180  
 Db 115 SSGGGSGGGSGGGSDVLMQTPLTSLTIGQPSLSCSSQSLDLS-DGTYTNMLL 173  
 QY 181 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKQSYNLPTF 239  
 Db 174 QKPGSPKVLIVASLDSGVDPDRFTGSGSGTDFTLKINRAEDLGVYVCMGTHSPLT 233  
 QY 240 FGGTKLEIK 249  
 Db 234 FGGTKLEIK 243  
 RESULT 5  
 AAM28491  
 ID AAM28491 standard; protein; 535 AA.  
 AC AAM28491;  
 XX  
 DT 25-NOV-1997 (first entry)  
 DE Human p53 protein variant S-325 encoded by p5C176.  
 XX  
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV,  
 KW anti-oncogene; hyperproliferation; cancer; re-stenosis; ScFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.  
 XX  
 OS Homo sapiens.  
 OS Herpes simplex virus.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 PN WO9704092-A1.  
 PD 06-FEB-1997.  
 XX  
 PF 17-JUL-1996; 96WO-FR001111.  
 XX  
 PR 19-JUL-1995; 95FR-00008729.  
 XX  
 PA (RHON ) RHONE POULENC RORER SA.

PI Conseller E, Bracco L;  
 XX  
 DR WPI: 1997-132633/12.  
 DR N-PSDB; AAT86221.  
 XX  
 PT New p53 variants e.g. with oligomerisation domain replaced by leucine  
 PT zipper - useful for treating hyper-proliferative disorders, esp. cancer  
 PT and restenosis.  
 XX  
 PS Claim 36; Page 88-90; 133pp; French.  
 CC Claimed variants of protein p53 have at least part of the oligomerisation  
 CC domain deleted and replaced by a leucine zipper domain. The mutants  
 CC preferably also have at least part of the p53 transactivation domain  
 CC (amino acids 1-74) deleted and replaced by the transactivating domain  
 CC (TAD) from herpes simplex virus viral protein VP16 (amino acids 411-490)  
 CC or by a protein domain able to bind selectively to a transactivator,  
 CC especially a single-chain antibody variable domain (ScFv). The present  
 CC sequence is that of a specifically claimed p53 variant designated S-325  
 CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53  
 CC and a leucine zipper domain at the C-terminal. The p53 variants are more  
 CC active and more stable tumour suppressors and apoptosis-inducing agents  
 CC than wild-type p53 and are active where the wild-type protein is not,  
 CC i.e. they are not inactivated by dominant negative or oncogenic mutants,  
 CC nor by other cellular proteins (because the leucine zipper domain  
 CC prevents formation of inactive mixed oligomers)  
 CC  
 XX Sequence 535 AA;  
 SQ  
 Query Match 72.6%; Score 955; DB 2; Length 535;  
 Best Local Similarity 74.4%; Pred. No. 4.1e-61;  
 Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;  
 QY 1 QVKLOESGAEIVSGASVNLSTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 60  
 Db 3 QVQLQESGAEIVSGASVNLSTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 62  
 QY 61 APNFQKATVTADTSSNTAVYHLSLTSEPTVYVCNAVYYEYDGYALDYWGQGTIVTV 120  
 Db 63 APKFGKATMTADTSSNTAVYHLSLTSEPTVYVCNAVYYEYDGYALDYWGQGTIVTV 116  
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLYASAGKVMCKSSQSLNFRKXYLYAMQ 180  
 Db 117 SSGGGSGGGSGGGSGGSDVLTQTPPLTSLVTIGQPAISCKSSQSLNDS-DGKTYLWML 175  
 QY 181 QKPGQSPKVLITWMASTRESGVDPDRFTSGSGTDFTLTITSSVQADFLAVYYCKQSNLP-T 239  
 Db 176 QRPQOSPRKLITLYLVSKLDSGVDPDRFTSGSGTDFTLTINRVAEDLIGVYYCMQGTHTSPLT 235  
 QY 240 FGGGTKLEIK 249  
 Db 236 FGAQTKLELK 245  
 RESULT 6  
 AAM28492 standard; protein; 535 AA.  
 ID AAM28492;  
 AC AAM28492;  
 XX  
 DT 25-NOV-1997 (first entry)  
 DE Human p53 protein variant S-325H.  
 XX  
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;  
 KW substitution; replacement; transactivation; viral protein VP16; HSV;  
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;  
 KW tumour suppression; apoptosis; single chain antibody variable domain.  
 XX  
 OS Homo sapiens.  
 OS Herpes simplex virus.  
 OS Synthetic.  
 OS Chimeric.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 361  
 FT /note= "Arg residue at position 182 of wild-type p53 has  
 FT been mutated to His"  
 FT  
 XX WO9704092-A1.  
 XX  
 XX 06-FEB-1997.  
 XX  
 XX 17-JUL-1996; 96WO-FR001111.  
 XX  
 XX 19-JUL-1995; 95FR-00008729.  
 XX  
 XX (RHON ) RHONE POUJENC RORER SA.  
 XX  
 XX Conseller E, Bracco L;  
 XX  
 XX WPI: 1997-132633/12.  
 XX  
 XX  
 XX New p53 variants e.g. with oligomerisation domain replaced by leucine  
 XX zipper - useful for treating hyper-proliferative disorders, esp. cancer  
 XX and restenosis.  
 XX  
 XX Claim 36; Page; 133pp; French.  
 XX  
 CC Claimed variants of protein p53 have at least part of the oligomerisation  
 CC domain deleted and replaced by a leucine zipper domain. The mutants  
 CC preferably also have at least part of the p53 transactivation domain  
 CC (amino acids 1-74) deleted and replaced by the transactivating domain  
 CC (TAD) from herpes simplex virus viral protein VP16 (amino acids 411-490)  
 CC or by a protein domain able to bind selectively to a transactivator,  
 CC especially a single-chain antibody variable domain (ScFv). The present  
 CC sequence is that of a specifically claimed p53 variant designated S-325H  
 CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53  
 CC (but with Arg182 replaced by His) and a leucine zipper domain at the C-  
 CC terminal. The p53 variants are more active and more stable tumour  
 CC suppressors and apoptosis-inducing agents than wild-type p53 and are  
 CC active where the wild-type protein is not, i.e. they are not inactivated  
 CC by dominant negative or oncogenic mutants, nor by other cellular proteins  
 CC (because the leucine zipper domain prevents formation of inactive mixed  
 CC oligomers). (Note: this sequence does not appear in the specification and  
 CC has been produced by modifying the given sequence of variant V-325)  
 CC  
 XX Sequence 535 AA;  
 SQ  
 Query Match 72.6%; Score 955; DB 2; Length 535;  
 Best Local Similarity 74.4%; Pred. No. 4.1e-61;  
 Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;  
 QY 1 QVKLOESGAEIVSGASVNLSTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 60  
 Db 3 QVQLQESGAEIVSGASVNLSTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 62  
 QY 61 APNFQKATVTADTSSNTAVYHLSLTSEPTVYVCNAVYYEYDGYALDYWGQGTIVTV 120  
 Db 63 APKFGKATMTADTSSNTAVYHLSLTSEPTVYVCNAVYYEYDGYALDYWGQGTIVTV 116  
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLYASAGKVMCKSSQSLNFRKXYLYAMQ 180  
 Db 117 SSGGGSGGGSGGGSGGSDVLTQTPPLTSLVTIGQPAISCKSSQSLNDS-DGKTYLWML 175  
 QY 181 QKPGQSPKVLITWMASTRESGVDPDRFTSGSGTDFTLTITSSVQADFLAVYYCKQSNLP-T 239  
 Db 176 QRPQOSPRKLITLYLVSKLDSGVDPDRFTSGSGTDFTLTINRVAEDLIGVYYCMQGTHTSPLT 235  
 QY 240 FGGGTKLEIK 249  
 Db 236 FGAQTKLELK 245  
 RESULT 7  
 AAM90217



ID	AAW90217	standard; protein; 580 AA.
XX		
AC	AAW90217;	
XX		
DT	10-MAY-1999	(first entry)
XX		
DE	Bispecific tetraivalent antibody B1r7AB7-24-1G10H6.	
XX		
KW	B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;	
KW	T cell activation; inhibitor; graft versus host disease;	
KW	transplant rejection; allograft rejection; autoimmune disease; allergy;	
KW	therapy; human; bispecific tetraivalent antibody; B1r7AB7-24-1G10H6.	
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Synthetic.	
OS	Chimeric.	
XX		
Key	Location/Qualifiers	
FT	Peptide	1..24
FT		/note= "pe1B signal peptide"
FT	Region	25..138
FT		/note= "VH region anti B7.1 MAb"
FT	Peptide	139..153
FT		/note= "(G4S3) flexible linker"
FT	Region	154..262
FT		/note= "VL region anti B7.1 MAb"
FT	Misc-difference	261
FT		/note= "encoded by CTG"
FT	Region	263..273
FT		/note= "human IgG3 hinge region"
FT	Domain	274..308
FT		/note= "helix-turn-helix dimerisation domain"
FT	Domain	309..319
FT		/note= "human IgG3 hinge domain"
FT	Region	320..446
FT		/note= "VH region anti B7.2 MAB"
FT	Misc-difference	322..327
FT		/note= "codons for these amino acids are not present in the DNA sequence for B1r7AB7-24-1G1-H6 provided in the specification"
FT	Peptide	447..461
FT		/note= "(G4S3) flexible linker"
FT	Region	462..574
FT		/note= "VL region anti B7.2 MAB"
FT	Peptide	575..580
FT		/note= "His6 tag"
XX		
PN	W09858965-A2.	
XX		
PD	30-DEC-1998.	
XX		
XX	22-JUN-1998;	98WO-EP003791.
XX		
PR	20-JUN-1997;	97EP-00870092.
XX		
PA	(INNO-) INNOGENETICS NV.	
XX		
PI	Lorre K, Sablon E, Buysse M, Bosman A;	
XX		
DR	WPI; 1999-105615/09.	
DR	N-PSDB; AAX01651.	
XX		
XX		
PT	New molecules which bind B7.1 and B7.2 - useful to prevent and treat	
PT	immune diseases including allograft rejection.	
XX		
PS	Example 7.1; Fig 16; 182pp; English.	
CC		
CC	This polypeptide comprises the bispecific tetraivalent antibody B1r7AB7-24-	
CC	-1G10H6. The molecule consists of 4 scfvs, i.e. 2 anti B7.1 scfvs and 2	
CC	anti B7.2 scfvs (tetravalency). One single B1r7AB is a homodimer of 2	
CC	identical molecules, each containing both an anti B7.1 and anti B7.2 scfv	

(bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a dimerisation domain (see AAW90219), which drives the homodimerisation of the molecule. DNA (see AAX01651) encoding the B7rAb has been constructed to allow expression of the B7rAb in transformed E. coli cells. The B7rAb cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigen-presenting cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed).

SQ Sequence 580 AA:

	Query March	72.3%;	Score 951;	D8 2;	Length 580;
	Best Local Similarity	73.5%;	Pred. No. 8.	8e-61;	
	Matches 183;	Conservative 22;	Mismatches 44;	Indels 0;	Gaps 0;
QY	1 QVKLQSGAEILVRSGASVNLCTASGPNIKIDYYMHWKORPEEGLEWIGYIDPESGETEY	60			
Db	325 QVOLQSGPEPLEEKPGASVTKISCKRSGAGSYFTGHNNMWKQNSKGSLIEWIGILDIPYGGSITSY	384			
QY	61 APNPKGATYADTDSNSTAYLIHLSLTISEPTITTYCNAAVLYYEDDGAALDYWGQGTIVTV	120			
Db	385 NPKEGAKTLIVDSSSTAHWLBSLTSEDSASAVIYCRRPAYICGYITIMYMGOGITIVTV	444			
QY	121 SSGGGSGSGGGGGGSDIELTOSPSLLAVSAGEKYAMSCKSQSOSLFNSRTKKNYLAHQ	180			
Db	445 SSGGGSGSGGGGGGSDIELTOSPSLLAVSAGEEVTMTCKSSQSVALYSNOKUYLAHQ	504			
QY	181 QKPQSPKVLITYMASTRSGVPDPFTSGSGTGTPETLTIISSVOAEDLNAVYCKQSNYNLPTE	240			
Db	505 QKPQSPKLLITYMASTRSGVPDRFRTSGSGTDPSLTIISSVOAEDLNAVYCHQYLSSWT	564			
QY	241 GGGTKLEIK 249				
Db	565 GGGTKLEIK 573				

RESULT 8
AAW90218
ID AAW90218 standard; protein; 556 AA.
XX
XX AC AAW90218;
XX
DT 10-MAY-1999 (first entry)
DE Bispecific tetraivalent antibody B17Ab1G10-B7-24H6.
XX
KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; bispecific tetraivalent antibody; B17Ab; B17Ab1G10-B7-24H6.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key
FT Region
FT     location/Qualifiers
FT         1..120
FT         /note= "VH region anti B7.2 Mab"
FT     Peptide
FT         121..135
FT         /note= "(G4S3) flexible linker"
FT     Region
FT         136..248
FT         /note= "VL region anti B7.2 Mab"
FT     Region
FT         249..259
FT         /note= "human IgG3 hinge region"
FT     Domain
FT         260..285
FT         /note= "helix-turn-helix dimerisation domain"
FT     Domain
FT         286..305
FT         /note= "human IgG3 hinge domain"

FT Region 306..426  
 FT /note="VH region anti B7.1 Mab"  
 FT Peptide 427..441  
 FT /note="G4S3 flexible linker"  
 FT Region 442..550  
 FT /note="VL region anti B7.1 Mab"  
 FT Peptide 551..556  
 FT /note="His6 tag"  
 XX  
 XX MO9658965-A2.  
 XX  
 XX 30-DEC-1998.  
 XX  
 XX 22-JUN-1998; 98MO-BP003791.  
 XX PF  
 XX 20-JUN-1997; 97EP-00870092.  
 XX PR  
 XX (INNO-) INNOGENETICS NV.  
 XX PA  
 XX Lorre K, Sablon E, Buysse M, Bosman A;  
 XX PI  
 XX WPI; 1999-105615/09.  
 XX DR  
 XX N-PSDB; AAX01652.  
 XX  
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection.  
 XX  
 PS Example 7.1; Fig 18; 182pp; English.  
 XX

CC This polypeptide comprises the bispecific tetraivalent antibody B17b1G10-  
 CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2  
 CC anti B7.2 scFvs (tetravalency). One single B17b is a homodimer of 2  
 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv  
 CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a  
 CC dimerisation domain (see AAM90219), which drives the homodimerisation of  
 CC the molecule. DNA (see AAX01652) encoding the B17b has been constructed  
 CC to allow expression of the B17b in transformed E. coli cells. The B17b  
 CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1  
 CC and B7.2 that are expressed on the membrane of professional antigen-  
 CC presenting cells, leading to the inhibition of antigen-specific T cell  
 CC activation. The invention relates to such B7-binding molecules, methods  
 CC for their production, and their use for treating or preventing diseases  
 CC of the immune system, in particular graft rejection, graft versus host  
 CC disease, allergy and autoimmune diseases (claimed)  
 CC  
 XX

SQ Sequence 556 AA;

Query Match 71.6%; Score 942; DB 2; Length 556;  
 Best Local Similarity 73.3%; Pred. No. 3.8e-60;  
 Matches 181; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

QY 3 KLOESGAEIVRSAGAVNLSCTASGENIKDYMHWMKQREBGLMWTGYIDPESGETEYAP 62  
 DB 1 QLOESGAEIVRSAGAVNLSCTASGENIKDYMHWMKQREBGLMWTGYIDPESGETEYAP 60  
 QY 63 NFOGKATVTAADSSNNAYLHLSLTSEPTTVYYCNNAVITYEYGYALDWYGGTIVTVSS 122  
 DB 61 KFBGKATLTVDKSSSTAYWQLSLTSEDSAVYICARFAYIGYIIMDYGGTIVTVSS 120  
 QY 123 GGGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQOK 182  
 DB 121 GGGGGGGGGGGGGSDIELTQSPSSILAVSAGEVMTCKSSQSVLYSSNOKRYLAWYQOK 180  
 QY 133 PGQSGKVLIVMASTESGVPRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLPTRGG 242  
 DB 181 PGQSGKVLIVMASTESGVPRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLPTRGG 240  
 QY 243 GTKLEIK 249  
 DB 241 GTKLEIK 247

RESULT 9

AAW37738  
 ID AAW37738 standard; protein; 437 AA.

XX AAW37738;

AC 17-OCT-2003 (revised)  
 DT 07-JUL-1998 (first entry)  
 XX

DE Nucleotide sequence encoding the Mgr6-clavin immunotoxin.

XX Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition;  
 XX protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent.

OS Aspergillus clavatus.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 96..286  
 FT /note="Mgr6 from M. musculus"

FT Peptide 287..437  
 FT /note="Clavin from A. clavatus"

XX MO9749726-A1.

XX 31-DEC-1997.

XX 26-JUN-1997; 97WO-BP003359.

XX 27-JUN-1996; 96IT-FI000155.

XX (ITVY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX Mele A, De Santis R, Parente D, Cologni M;

XX WPI; 1998-077109/07.

XX DR N-PSDB; AAW09256.

XX DNA encoding Aspergillus clavatus-derived ribosomal inhibitor protein,  
 PT clavin - useful as an immuno-conjugate and for treatment of cancer.

PS Claim 4; Page 14-15; 26pp; English.

CC This is the amino acid sequence of a fusion protein comprising of the Mgr6  
 CC single chain antibody (with the heavy and light chain joined by a  
 CC linker), fused to the clavin protein. Clavin is an inhibitor protein, and  
 CC functions by inactivating the ribosomes. Clavin or its conjugates are  
 CC useful as anticancer and/or antiviral agents. The recombinant ribosomal  
 CC inhibitor protein (RIP), Mgr6-clavin (a conjugate of clavin) is used as  
 CC an immunoconjugate, and the complex and clavin alone are capable of  
 CC inhibiting ribosomal activity. (Updated on 17-OCT-2003 to standardise OS  
 CC field)

SQ Sequence 437 AA;

Query Match 70.9%; Score 932.5; DB 2; Length 437;  
 Best Local Similarity 72.8%; Pred. No. 1.4e-59;  
 Matches 182; Conservative 25; Mismatches 36; Indels 7; Gaps 4;

QY 1 QYKLOESGAEIVRSAGAVNLSCTASGENIKDYMHWMKQREBGLMWTGYIDPESGETEY 60  
 DB 37 QYKLOESGAEIVRSAGAVNLSCTASGENIKDYMHWMKQREBGLMWTGYIDPESGETEY 96  
 QY 61 APNFGKATVTAADSSNNAYLHLSLTSEPTTVYYCNNAVITYEYGYALDWYGGTIVTV 120  
 DB 97 DPKEFGKATVTAADSSNNAYLHLSLTSEPTTVYYCNNAVITYEYGYALDWYGGTIVTV 152  
 QY 121 SSGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQ 180  
 DB 153 SSGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQ 210  
 QY 181 QKPGSPKVLIVMASTESGVPRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLP-T 239  
 DB 181 QKPGSPKVLIVMASTESGVPRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLP-T 239

Db 211 OKGPPKLLIKYASNLSEGVAPRRSGSGSTDTLTINHPVEEDTATYTCOHSWEIPRT 270  
 QY 240 FGGATKLEIK 249  
 Db 271 FGGATKLEIK 280

RESULT 10  
 AAU72865  
 ID AAU72865 standard; protein; 258 AA.

AC AAU72865;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE P5-2 single chain Fv.  
 XX  
 KW Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour;  
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;  
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;  
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;  
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DA10;  
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;  
 KW 8G7C10; 6ESA7; 11B2D10x4-7; 8G7C10x4-7; 6ESA7x4-7; P4-2; P4-3; P4-14;  
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;  
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.  
 XX  
 OS Homo sapiens.  
 XX  
 EN WO200171005-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 26-MAR-2001; 2001WO-EP003414.  
 XX  
 PR 24-MAR-2000; 2000EP-00106467.  
 XX  
 PA (KUFE/) KUFER P.  
 XX  
 PI Kufner P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;  
 PI Mayer M, Hofmeister R;  
 DR WPI; 2002-055119/07.  
 DR N-PSDB; AAS971139.  
 XX

PT Multifunctional polypeptides comprising binding sites that specifically  
 PT recognize extracellular groups of the NKGD2 receptor complex and domains  
 PT which function as receptors or ligands, useful for treating cancers and  
 PT infectious diseases.  
 XX

XX Example 7; Fig 16; 11app; English.  
 XX

XX The invention relates to a multifunctional polypeptide comprising a  
 CC domain with a binding site that specifically recognises an extracellular  
 CC group of the NKGD2 receptor complex and a second domain which functions  
 CC as a receptor or ligand. The polypeptide and its associated  
 CC polynucleotide are used for the preparation of a pharmaceutical  
 CC composition for the treatment of cancer, infections and/or autoimmune  
 CC conditions. The cancer may be a tumour of the head and neck, stomach,  
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,  
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,  
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.  
 CC The infectious diseases can be caused by viruses, bacteria, fungi,  
 CC protozoa or helminths. The autoimmune diseases include multiple  
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior  
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent  
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and  
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKGD2  
 CC receptor and the polypeptides of the invention  
 XX

XX Sequence 258 AA;  
 XX

Query Match 70.8%; Score 931; DB 5; Length 258;

Best Local Similarity 72.5%; Pred. No. 1e-59;  
 Matches 179; Conservative 22; Mismatches 40; Indels 6; Gaps 2;

QY 4 LOESGAEIVRSQASVNSCTASGNIKDYMMWVKORPEGLIEWIGYIDPESGETEYAPN 63  
 Db 5 LEQSGAEIMKPGASVKISCKATGYTFSSYIEWVKORPGHGLEWIGILPSSGSTNNYNEK 64  
 QY 64 FQKATVTADTSSMTAVYMHLSLTSEPTTYVCNAVYYEDGALDVPWGQGTYYVSSG 123  
 Db 65 FKGATFTADTSSMTAVYMQSLTSEDSAVYVCARGLRWF-----AWGQGTYYVSSG 119  
 QY 124 GGSGGGGGGSDIELTGSSSLAVSAGEKVMSCSSQSLFNSRTRKXYLAHYQXP 183  
 Db 120 GGSGGGGGGGGSELVMTGQSPSSILTYAGKVMSCSSQSLNSGQXVLYTYQXP 179  
 QY 184 GQSPKVIILYMASTRESGVDPDRFTGSGGTDFTLTITSSVQABDLAVYYCKQSYNP-P-TPGG 242  
 Db 180 GQPKVILYMASTRESGVDPDRFTGSGGTDFTLTITSSVQABDLAVYYCQNDYSYDLTFGA 239  
 QY 243 GTKLEIK 249  
 Db 240 GTKLEIK 246

RESULT 11  
 AA117960  
 ID AA117960 standard; protein; 248 AA.  
 XX  
 AC AA117960;  
 XX  
 DT 04-AUG-1999 (first entry)  
 XX  
 DE Mouse scFv fragment 4-1.  
 XX  
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;  
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.  
 XX  
 OS Mus sp.  
 XX  
 EN WO9925818-A1.  
 XX  
 PD 27-MAY-1999.  
 XX  
 PF 16-NOV-1998; 98WO-EP007313.  
 XX  
 PR 17-NOV-1997; 97EP-00120096.  
 XX  
 PA (KUFE/) KUFER P.  
 XX

PI Kufner P, Raum T, Borschert K, Zettl F, Lutterbuese R;  
 PI WPI; 1999-338004/28.  
 DR N-PSDB; AAX77243.  
 XX

PT Phase display system for identification of binding site domains retaining  
 PT capacity to bind an epitope.  
 XX

XX Claim 27; Fig 6.6; 152pp; English.  
 XX

XX The invention relates to a method of identifying binding site domains  
 CC (BSD) that retain the capacity of binding to a predetermined epitope when  
 CC positioned C-terminal of at least one further domain in a recombinant bi-  
 CC or multivalent polypeptide. The method comprises (a) testing a panel of  
 CC BSD displayed on the surface of a biological display system as part of a  
 CC fusion protein for binding to a predetermined epitope, where the fusion  
 CC protein comprises an additional domain positioned N-terminal of the BSD  
 CC and an amino acid sequence that mediates anchoring of the fusion protein  
 CC to the surface of the display system; and (b) identifying a BSD that  
 CC binds to the predetermined epitope. The method is useful to identify bi-  
 CC or multivalent polypeptides that comprise antibody binding sites capable  
 CC of efficiently binding to the corresponding antigen. The polypeptides or  
 CC antibodies identified by the method are useful therapeutically and  
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody

fragments that bind independently of their position within bifunctional single-chain fusion proteins can be isolated from combinatorial antibody libraries using the new in vitro method. Sequences AAY1757-965 represent mouse scFv fragments

Sequence 248 AA;  
Query Match 70.7%; Score 930; DB 2; Length 248;  
Best Local Similarity 72.9%; Pred. No. 1.2e-59;  
Matches 180; Conservative 25; Mismatches 38; Indels 4; Gaps 2;

```
OY 4 LOESGAEIVRSASVNLCTASGFNIKDYMHVMWKQREEGLEWIGYIDPSGETEYAPN 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 LEQSAELVREPTGSKISCKASGYAFTHYWLQWVRGHEHFWGDLFPSSGNHAYEK 64
OY 64 FQKATVTADTSNTAVYHLISLTSEDITVYVCNAVYYEYDGVALDYWGQGTIVTV 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 FKGKATLTADKSSYTAVMQLSLTSEDGAVVFCALRWMD--EAMDYWGQGTIVTVSSG 121
OY 124 GGGSGGGSGGGSGDIETQSPSSLAASAGEKVMSCSSQSLFNSRIRKNTLAWYQKP 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 GGGSGGGSGGGSGELVMTQSPSSLSVSAKEKVTSCSSQSLNSGNQNTLAWYQKP 181
OY 184 GQSPKVLTYMASTRSGVDPDRFTGSGGTDFTLTITSSVQAEIDLAVYCKOSYNLP-TEGG 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 GQPKLLTYGASTRSGVDPDRFTGSGGTDFTLTITSSVQAEIDLAVYCKQNDYSPFTTGG 241
OY 243 GTKLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 242 GTKLEIK 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 12

ABJ26742 ID ABJ26742 standard; protein; 240 AA.

XX ABJ26742;

XX 01-MAY-2003 (first entry)

XX VEGF binding related protein SEQ ID No 51.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;

XX leukaemia cell; vascular endothelial growth factor; tumour;

XX bispecific antigen-binding protein; mouse; murine.

XX Mus sp.

XX WO2003002144-A1.

XX 09-JAN-2003.

XX 26-JUN-2002; 2002WO-US020332.

XX 26-JUN-2001; 2001US-0301299P.

XX (IMCL-) IMCLONE SYSTEMS INC.

XX Zhu Z;

XX WPI; 2003-201468/19.

XX N-PSDB; ABR23322.

XX New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors.

XX Disclosure; Page 63; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF)

XX receptor and a second antigen-binding site specific for a second VEGF

receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention

Sequence 240 AA;  
Query Match 70.3%; Score 924.5; DB 6; Length 240;  
Best Local Similarity 71.2%; Pred. No. 2.8e-59;  
Matches 178; Conservative 27; Mismatches 32; Indels 13; Gaps 3;

```
OY 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHVMWKQREEGLEWIGYIDPSGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHVMWKQREEGLEWIGYIDPSGETEY 60
OY 61 APNFGKATVTADTSNTAVYHLISLTSEDITVYVCNAVYYEYDGVALDYWGQGTIVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DPKFGKATLTADTSNTAVYHLISLTSEDITVYVCNAVYYCALPPY-----FDYWGHEGTIVTV 114
OY 121 SSGSGSGGGSGGGSGDIETQSPSSLAASAGEKVMSCSSQSLFNSRIRKNTLAWYQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 SSGSGSGGGSGGGSGDIETQSPSSLAASAGEKVMSCSSQSLFNSRIRKNTLAWYQ 168
OY 181 QKPGSPKVLTYMASTRSGVDPDRFTGSGGTDFTLTITSSVQAEIDLAVYCKOSYNLP-T 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 169 QKPGSPKALTYMASRYSGVDPDRFTGSGGTDFTLTITSSVQAEIDLAVYCKQNDYSPFTT 228
OY 240 FGGGTLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 229 FGGGTLEIK 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 13

AAB31422 ID AAB31422 standard; protein; 242 AA.

XX AAB31422;

XX 20-APR-2001 (first entry)

XX Protein used for immunising against shed antigen-specific B cells.

XX Vaccine; shed antigen-specific B cell; idiotypic antibody;

XX immune complex-mediated disease; autoimmune disease;

XX humoral immune response; cancer.

XX Synthetic.

XX WO200076319-A1.

XX 21-DEC-2000.

XX 16-JUN-2000; 2000WO-US016677.

XX 16-JUN-1999; 99US-0139521P.

XX 15-JUN-2000; 2000US-00594985.

XX (BIOC-) BIOCRYSTAL LTD.

XX Nelson MB, Barbera-Guillem E;

XX WPI; 2001-080635/09.

XX Inducing an immune response against shed antigen-specific B cell

XX idiotypes, by administering a vaccine formulation comprising

XX polynucleotides encoding an idiotypic determinant or peptides comprising

XX an idiotypic determinant.

XX Example 2; Page 66-67; 81pp; English.

CC The present sequence represents a synthetic protein which may be used in  
 CC vaccines for inducing immune responses of the invention. The protein  
 CC comprises a VH region linked to a VL region. The specification describes  
 CC a method for inducing an immune response reactive with idiotypes present  
 CC on shed antigen-specific B cells (SAB) of an individual. The method  
 CC involves administering a vaccine formulation comprising polynucleotide  
 CC encoding an idiotype of an antibody that binds to an epitope of shed  
 CC antigen. The method is useful for inducing an immune response reactive  
 CC with idiotypes present on SAB of an individual. The method is useful for  
 CC depleting shed antigen-specific B cells, and for treating immune complex-  
 CC mediated disease progression in organ specific autoimmune disease  
 CC exacerbated by humoral immune response against groups expressed on shed  
 CC antigen, or by plasma cell production of antibodies against groups of  
 CC shed antigen. It is useful in cancer therapy and for treating autoimmune  
 CC disease

XX Sequence 242 AA;

Query Match 70.2%; Score 923.5; DB 4; Length 242;

Best Local Similarity 70.0%; Pred. No. 3.4e-59;

Matches 175; Conservative 29; Mismatches 37; Indels 9; Gaps 2;

QY 1 QVKLQESGALVPSGASVNSCTASGFNIKDYVMHWKORPEBGLWIGYIDPESGETEY 60  
 Db 1 QVQLQESGALVPSGASVNSCTASGFNIKDYVMHWKORPEBGLWIGYIDPESGETEY 60  
 QY 61 AEPNQGKATVADTSSNTAYLHLSTLSEDTVTYYCNNAVYYEDYALDYWGQGTFTVY 120  
 Db 61 NEKFKGKATLTADKSSSTAYVQNLSTSEDSAVYFCRSYY-----GHMGGTITVY 112  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 180  
 Db 113 SSGGGSGGGSGGGSDIYMSQSPSSLPVSGEKVTLSCKSSQSLTSGNQKNYLAAYQ 172  
 QY 181 QKPGSPKVLIVYASTRESGVDPFRFTSGSGTDFTLTSSVQAEDLAAYYCKQSYNLP-T 239  
 Db 173 QKPGSPKVLIVYASTRESGVDPFRFTSGSGTDFTLTSSVQAEDLAAYYCKQSYNLP-T 232  
 QY 240 FGGGTKEIK 249  
 Db 233 FGGGTKEIK 242

RESULT 14

AA17964 ID AA17964 standard; protein; 248 AA.

AC AA17964;

DT 04-AUG-1999 (first entry)

DE Mouse scFv fragment 5-10.

KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;

KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.

OS Mus sp.

PN WO9925818-A1.

PD 27-MAY-1999.

PF 16-NOV-1998; 98WO-BP007313.

PR 17-NOV-1997; 97EP-00120096.

PA (KUEF) KUEP P.

PI Kufer P, Raum T, Borschert K, Zetl F, Lutterbuese R;

DR WPI; 1999-338004/28.

DR N-PSDB; AAX77247.

XX

PT Phage display system for identification of binding site domains retaining  
 PT capacity to bind an epitope.

PS Claim 27, Fig 6.10; 152pp; English.

XX The invention relates to a method of identifying binding site domains  
 CC (BSD) that retain the capacity of binding to a predetermined epitope when  
 CC positioned C-terminal of at least one further domain in a recombinant bi-  
 CC or multivalent polypeptide. The method comprises (a) testing a panel of  
 CC BSD displayed on the surface of a biological display system as part of a  
 CC fusion protein for binding to a predetermined epitope, where the fusion  
 CC protein comprises an additional domain positioned N-terminal of the BSD  
 CC and an amino acid sequence that mediates anchoring of the fusion protein  
 CC to the surface of the display system, and (b) identifying a BSD that  
 CC binds to the predetermined epitope. The method is useful to identify bi-  
 CC or multivalent polypeptides that comprise antibody binding sites capable  
 CC of efficiently binding to the corresponding antigen. The polypeptides or  
 CC antibodies identified by the method are useful therapeutically and  
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody  
 CC fragments that bind independently of their position within bifunctional  
 CC single-chain fusion proteins can be isolated from combinatorial antibody  
 CC libraries using the new in vitro method. Sequences AA17957-965 represent  
 CC mouse scFv fragments

XX Sequence 248 AA;

Query Match 70.0%; Score 921; DB 2; Length 248;

Best Local Similarity 71.7%; Pred. No. 5.2e-59;

Matches 177; Conservative 25; Mismatches 41; Indels 4; Gaps 2;

QY 4 LQESGAEIVRSASVNSCTASGFNIKDYVMHWKORPEBGLWIGYIDPESGETEAPN 63  
 Db 5 LQESGAEIVRPSGASVNSCTASGFNTNWLGMWKORPGHGLEIDIFPGSGNHNEX 64  
 QY 64 FQKATVADTSSNTAYLHLSTLSEDTVTYYCNNAVYYEDYALDYWGQGTFTVYSSG 123  
 Db 65 FQKATLTADKSSSTAYVQNLSTSEDSAVYFCARLRMD---EPMDYWGQGTFTVYSSG 121  
 QY 124 GGGSGGGSGGGSDIELTQSPSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQOKP 183  
 Db 122 GGGSGGGSGGGSDIYMSQSPSSLPVSGEKVTLSCKSSQSLTSGNQKNYLAAYQOKP 181  
 QY 184 GQSPKVLIVYASTRESGVDPFRFTSGSGTDFTLTSSVQAEDLAAYYCKQSYNLP-TFGG 242  
 Db 182 GQPPKVLIVYASTRESGVDPFRFTSGSGTDFTLTSSVQAEDLAAYYCKQSYNLP-TFGA 241  
 QY 243 GTKLEIK 249  
 Db 242 GTKLEIK 248

RESULT 15

AAE25963 ID AAE25963 standard; protein; 238 AA.

AC AAE25963;

DT 15-NOV-2002 (first entry)

DE KDR binding immunoglobulin related mouse protein #3.

KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;

KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;

KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;

XX pIC11; scFv antibody.

OS Mus sp.

PN US2002064528-A1.

PD 30-MAY-2002.

DR 12-OCT-2001; 2001US-00976787.

XX

```
XX
PR 28-JAN-2000; 2000US-00493539.
XX
XX (ZHUZ/) ZHU Z.
PA (WITTE/) WITTE L.
XX
XX Zhu Z, Witte L;
PI
XX
DR WPI; 2002-589175/63.
XX
PT Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
PT insert domain-containing receptor with an affinity comparable to human
PT vascular endothelial growth factor, and neutralizes activation of KDR.
XX
PS Disclosure; Page 17-18; 34pp; English.
XX
CC The present invention relates to novel immunoglobulin molecules that bind
CC to kinase insert domain-containing receptor (KDR) (a human homologue of
CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
CC to human vascular endothelial growth factor (VEGF) and that neutralises
CC activation of KDR. Sequences of the invention are useful for neutralising
CC the activation of KDR, for reducing tumour growth and for inhibiting
CC angiogenesis. The present sequence is KDR binding immunoglobulin related
CC mouse protein
XX
SQ Sequence 238 AA;
XX
Query Match 69.8%; Score 917.5; DB 5; Length 238;
Best Local Similarity 70.4%; Pred. No. 9e-59;
Matches 176; Conservative 30; Mismatches 31; Indels 13; Gaps 4;
QY 1 QVKLOESGAEIVRSASVNLSTASGPNIKDYMHVWKQRPBEGLEWIGYIDPESGETEY 60
Db 1 QVKLOESGAEIVRSASVNLSTASGPNIKDYMHVWKQRPBEGLEWIGYIDPESGETEY 60
QY 61 APNFQGAITYTADTSSNTATYHLSLSEDTTYVCNAVITYEYDGYALDYGQGTIVTV 120
Db 61 APNFQGAITYTADTSSNTATYHLSLSEDTTYVCNAVITYEYDGYALDYGQGTIVTV 120
QY 61 APKFOGKATMTADSSNTAYIQLSLSEDTTAVYVCNA-YYGDTYEG---YWGQGTIVTV 115
Db 61 APKFOGKATMTADSSNTAYIQLSLSEDTTAVYVCNA-YYGDTYEG---YWGQGTIVTV 115
QY 121 SSGGGSGSGGGSGGGSDIELTQSPSSILAVSAGEKVMSCSKSOSLFNSRTRKNYLAWQ 180
Db 121 SSGGGSGSGGGSGGGSDIELTQSPSSILAVSAGEKVMSCSKSOSLFNSRTRKNYLAWQ 180
QY 116 SSGGGSGSGGGSGGGSDIELTQSPALMSASPGKVTITCSASSV-----SYMHWFQ 168
Db 116 SSGGGSGSGGGSGGGSDIELTQSPALMSASPGKVTITCSASSV-----SYMHWFQ 168
QY 181 QKPGQSPKVLITYMASTRSGVDRFTGSGGTDFTLTISVQAPDLAVYCKQSYNLP-T 239
Db 181 QKPGQSPKVLITYMASTRSGVDRFTGSGGTDFTLTISVQAPDLAVYCKQSYNLP-T 239
QY 169 QKPGTSPKVLITYSTSNLASGVPARFSGSGSTSYLTISRMEDADATYVQCQRSSYPFT 228
Db 169 QKPGTSPKVLITYSTSNLASGVPARFSGSGSTSYLTISRMEDADATYVQCQRSSYPFT 228
QY 240 FGGGTKLFIK 249
Db 240 FGGGTKLFIK 249
QY 229 FGGGTKLEIK 238
Db 229 FGGGTKLEIK 238
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Search completed: July 30, 2004, 11:19:21  
Job time : 50.0915 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:17:36 ; Search time 14.6768 Seconds  
(without alignments)  
875.861 Million cell updates/sec

Title: US-09-297-181-4  
Perfect score: 1215

Sequence: 1 QVKLQESGAEIVRGSVNL.....YCKQSYNLPTFGGTTLEIK 249

Scoring table: BLOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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IssueParents AA:*
1: /cgn2_6/prodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PTOTUS.COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfilled.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1024.5	77.9	288	4	US-09-423-439-38	Sequence 38, App
2	1024.5	77.9	673	4	US-09-423-439-32	Sequence 32, App
3	955	72.6	535	4	US-08-983-035A-38	Sequence 36, App
4	906	68.9	281	4	US-09-423-439-44	Sequence 44, App
5	906	68.9	666	4	US-09-423-439-51	Sequence 51, App
6	883	67.1	282	2	US-08-652-507-2	Sequence 2, App
7	877.5	66.7	280	2	US-08-860-174A-10	Sequence 10, App
8	877	66.7	553	3	US-08-661-052-16	Sequence 16, App
9	877	66.7	553	2	US-09-188-082-16	Sequence 16, App
10	877	66.7	553	4	US-09-364-088-16	Sequence 16, App
11	877	66.7	553	4	US-09-102-716-16	Sequence 16, App
12	854	64.9	240	4	US-10-092-246-36	Sequence 36, App
13	846	64.9	248	4	US-09-649-063-23	Sequence 23, App
14	842.5	64.1	249	2	US-08-797-689-18	Sequence 18, App
15	842.5	64.1	249	4	US-09-984-186-18	Sequence 18, App
16	839	63.8	240	4	US-10-092-246-37	Sequence 37, App
17	837	63.7	240	4	US-10-092-246-35	Sequence 35, App
18	831.5	63.2	277	2	US-08-266-790-2	Sequence 2, App
19	830	63.1	269	3	US-08-626-665A-109	Sequence 109, App
20	823.5	62.6	244	2	US-08-553-497A-20	Sequence 20, App
21	818	62.2	301	2	US-08-661-052-14	Sequence 14, App
22	818	62.2	301	3	US-09-188-082-14	Sequence 14, App
23	818	62.2	301	4	US-09-364-088-14	Sequence 14, App
24	818	62.2	301	4	US-09-102-716-14	Sequence 14, App
25	813.5	61.9	242	2	US-08-553-497A-26	Sequence 26, App
26	811.5	61.7	246	2	US-08-553-497A-24	Sequence 24, App
27	808.5	61.5	244	2	US-08-553-497A-22	Sequence 22, App

28	807.5	61.4	482	4	US-09-59.039-03.1-6	Sequence 16, Appl
29	803.5	61.1	483	2	US-08-392.338A-19	Sequence 19, Appl
30	803.5	61.1	483	3	US-09-166.750-19	Sequence 19, Appl
31	803.5	61.1	483	3	US-09-166.099-19	Sequence 19, Appl
32	803.5	61.1	483	3	US-09-172.019-19	Sequence 19, Appl
33	803.5	61.1	483	3	US-09-166.099-19	Sequence 19, Appl
34	803.5	61.1	483	3	US-09-44.4-21.1-19	Sequence 19, Appl
35	800.5	60.9	242	2	US-08-553.497A-28	Sequence 28, Appl
36	799	60.8	240	4	US-10-092.24-34	Sequence 34, Appl
37	799	60.8	265	2	US-08-403.85-16	Sequence 16, Appl
38	798.5	60.7	239	4	US-10-092.24-33	Sequence 33, Appl
39	797	60.6	256	4	US-09-526.738A-2	Sequence 2, Appl
40	797	60.6	258	4	US-09-526.738A-4	Sequence 4, Appl
41	796	60.5	273	2	US-08-403.85-18	Sequence 18, Appl
42	795.5	60.5	244	4	US-09-244.365B-1	Sequence 1, Appl
43	794	60.4	361	4	US-09-646.028-12	Sequence 12, Appl
44	794	60.4	348	4	US-09-646.028-12	Sequence 12, Appl
45	790	60.1	297	4	US-09-486.814A-2	Sequence 2, Appl

## ALIGNMENTS

```

1      RESULT 1
2      US-09-423-439-38
3      ; Sequence 38, Application US/09423439
4      ; Patent No. 6339070
5      ; GENERAL INFORMATION:
6      APPLICANT: EMERY, Stephen Charles
7      BLAKEY, David Charles
8      TITLE OF INVENTION: CHEMICAL COMPOUNDS
9      NUMBER OF SEQUENCES: 60
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: Pillsbury Winthrop, L.L.P.
12     STREET: 1100 New York Ave., N.W.
13     CITY: Washington
14     STATE: D.C.
15     COUNTRY: U.S.A.
16     ZIP: 20005
17
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: MS Word
23
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/09/423,439
26     FILING DATE: 09-NO. 6339070-1999
27     CLASSIFICATION: <Unknown>
28
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: PCT/GB98/01294
31     FILING DATE: 05-MAY-1998
32     APPLICATION NUMBER: GB 9709421.3
33     FILING DATE: 10-MAY-1997
34
35     INFORMATION FOR SEQ ID NO: 38:
36     SEQUENCE CHARACTERISTICS:
37     LENGTH: 288 amino acids
38     TYPE: amino acid
39     STRANDEDNESS: single
40     TOPOLOGY: linear
41
42     MOLECULE TYPE: protein
43
44     SEQUENCE DESCRIPTION: SEQ ID NO: 38:
45
46     US-09-423-439-38
47
48     Query Match          77.9%; Score 1024.5; DB 4; Length 288;
49     Best Local Similarity 77.9%; Pred. No. 4,4e-78;
50     Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1
51
52     1  QVQLQSGAGELVIRSGAVYLCTAAGFNLIKDYMHMWRVQRPEGLGIEWTGYIDSSGETEY 60
53     23  QVQVLOQPGAEIVKPGASVQLSSCKAGGYFTGTGWIHWVQRGGQGLEWVGEVNPSTGRSDY 82
54     61  APNFGKATVTDTSNTAYLIHLSTSTSEDTTVVCNAVITYEVDGVALDVGAGGTTVTV 120

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Db 83 NEKFNKATLTVDKSSTTAYWQLSLTSEDSAVVYCARERAYGYDD-ANDYWGQGTIVTV 141  
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 180  
Db 142 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 201  
QY 181 QKPGSPKVLIIYMASTRSGVDPDRFTSGSGSDTFTLTISVQAEIDLAVYCKOSYINLPTE 240  
Db 202 QKPGSPKVLIIYMASTRSGVDPDRFTSGSGSDTFTLTISVQAEIDLAVYCKOSYINLPTE 261  
QY 241 GGGTKLEIK 249  
Db 262 GGGTKLEIK 270

RESULT 2  
US-09-423-439-32  
Sequence 32, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 673 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-423-439-32

Query Match 77.9%; Score 1024.5; DB 4; Length 673;  
Best Local Similarity 77.9%; Pred. No. 1.2e-77;  
Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 QVKLOESGAEIYVRSGASVNLSTASGFNIKIDYMHWMVKORPEGLIEWIGYIDPSSGELEY 60  
Db 20 QVQLDQPGAEIYVRKASVQLSCKASGYFTFGYTHWVQRGGQGLEIHWGAVNPSYGRSDY 79  
QY 61 APNFOGKATVADTSSNTAYLHLSSLTSEDTVVYCNNAVITYEYDGVALDYWGQGTIVTV 120  
Db 80 NEKFNKATLTVDKSSTTAYWQLSLTSEDSAVVYCARERAYGYDD-ANDYWGQGTIVTV 138  
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 180  
Db 139 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 198  
QY 181 QKPGSPKVLIIYMASTRSGVDPDRFTSGSGSDTFTLTISVQAEIDLAVYCKOSYINLPTE 240

Db 199 QKPGSPKVLIIYMASTRSGVDPDRFTSGSGSDTFTLTISVQAEIDLAVYCKOSYINLPTE 258  
QY 241 GGGTKLEIK 249  
Db 259 GGGTKLEIK 267

RESULT 3  
US-08-983-035A-38  
Sequence 38, Application US/08983035A  
Patent No. 6326464  
GENERAL INFORMATION:  
APPLICANT: CONSELLER, EMMANUEL  
BRACCO, LAURENT  
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL  
USSES THEREOF  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP  
STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,035A  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01111  
FILING DATE: 17-JUL-1996  
APPLICATION NUMBER: FR 95/08729  
FILING DATE: 19-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Strauss, William L.  
REGISTRATION NUMBER: 47,114  
REFERENCE/DOCKET NUMBER: 03804.0142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-983-035A-38

Query Match 72.6%; Score 955; DB 4; Length 535;  
Best Local Similarity 74.4%; Pred. No. 6.1e-72;  
Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;

QY 1 QVKLOESGAEIYVRSGASVNLSTASGFNIKIDYMHWMVKORPEGLIEWIGYIDPSSGELEY 60  
Db 3 QVQLDQPGAEIYVRKASVQLSCKASGYFTFGYTHWVQRGGQGLEIHWGAVNPSYGRSDY 62  
QY 61 APNFOGKATVADTSSNTAYLHLSSLTSEDTVVYCNNAVITYEYDGVALDYWGQGTIVTV 120  
Db 63 APKIQGKATVADTSSNTAYLQLSLASEDTAVYYCN-----PYGALDYWGQGTIVTV 116  
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAAYQ 180  
Db 117 SSGGGSGGGSGGGSDIVLMTQTPILTSVITIGQPAISICKSSQSLIDS-DKTYLNNLL 175  
QY 181 QKPGSPKVLIIYMASTRSGVDPDRFTSGSGSDTFTLTISVQAEIDLAVYCKOSYINLPTE 239



Db 176 ORPGSPKRLIYVSKLDSGVDPDRFTSGSGSTDTLTKINRVEADLGVYCWQSTHPLT 235  
QY 240 FGGGTKEIK 249  
Db 236 FGAGTKLEIK 245

RESULT 4  
US-09-423-439-44  
Sequence 44, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423 439  
FILING DATE: 09-May-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-May-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-May-1997  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-09-423-439-44

Query Match 68.9%; Score 906; DB 4; Length 281;  
Best Local Similarity 69.2%; Pred. No. 3, 4e-68;  
Matches 173; Conservative 30; Mismatches 37; Indels 10; Gaps 3;  
QY 1 OVKLQESGAEIVRSASVNLCTASGFNFKDYMMWVKORPEGLWIGYIDPESGETY 60  
Db 23 EVQLQDSGAEIVRSASVNLCTASGFNFKDYMMWVKORPEGLWIGYIDPESGETY 82  
QY 61 APNFGKATVTADTSNTAYLHLSSLTSEDVTYVYCNAYIYYEYDGYALDYWGQGTIVY 120  
Db 83 APKFRGKATLTADSSSNTAYLHLSSLTSEDVTYVYCHVLIYAGY--LAMDYWGQGTIVY 140  
QY 121 SSGGGSGGGGGGGSDIEILQSPSLAVSAGEKVMASCKSSQSLFNSRTKNTLYAYQ 180  
Db 141 SSGGGSGGGGGGGGGGSDIVLTQSPALMSASPGKEVTTTCSASSSV-----TYMHWFQ 193  
QY 181 QKPGSPKRLIYVSKLDSGVDPDRFTSGSGSTDTLTKINRVEADLGVYCWQSTHPLT 235  
Db 194 QKPGSPKRLIYVSKLDSGVDPDRFTSGSGSTDTLTKINRVEADLGVYCWQSTHPLT 253  
QY 240 FGGGTKEIK 249  
Db 254 FGAGTKLEIK 263

RESULT 5

US-09-423-439-51  
Sequence 51, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-May-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-May-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-May-1997  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 666 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-423-439-51

Query Match 68.9%; Score 906; DB 4; Length 666;  
Best Local Similarity 69.2%; Pred. No. 9, 8e-68;  
Matches 173; Conservative 30; Mismatches 37; Indels 10; Gaps 3;  
QY 1 OVKLQESGAEIVRSASVNLCTASGFNFKDYMMWVKORPEGLWIGYIDPESGETY 60  
Db 20 EVQLQDSGAEIVRSASVNLCTASGFNFKDYMMWVKORPEGLWIGYIDPESGETY 79  
QY 61 APNFGKATVTADTSNTAYLHLSSLTSEDVTYVYCNAYIYYEYDGYALDYWGQGTIVY 120  
Db 80 APKFRGKATLTADSSSNTAYLHLSSLTSEDVTYVYCHVLIYAGY--LAMDYWGQGTIVY 137  
QY 121 SSGGGSGGGGGGGSDIEILQSPSLAVSAGEKVMASCKSSQSLFNSRTKNTLYAYQ 180  
Db 138 SSGGGSGGGGGGGGGGSDIVLTQSPALMSASPGKEVTTTCSASSSV-----TYMHWFQ 190  
QY 181 QKPGSPKRLIYVSKLDSGVDPDRFTSGSGSTDTLTKINRVEADLGVYCWQSTHPLT 235  
Db 191 QKPGSPKRLIYVSKLDSGVDPDRFTSGSGSTDTLTKINRVEADLGVYCWQSTHPLT 250  
QY 240 FGGGTKEIK 249  
Db 251 FGAGTKLEIK 260

RESULT 6  
US-08-652-507-2  
Sequence 2, Application US/08652507  
Patent No. 5876691  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN  
NUMBER OF SEQUENCES: 8

```

CORRESPONDENCE ADDRESS:
ADDRESS: Nixon & Vandehy, P.C.
STREET: 1100 No. 587691th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-2

```

```

Query Match      67.1%; Score 883; DB 2; Length 270;
Best Local Similarity 67.1%; Pred. No. 2,7e-66;
Matches 171; Conservative 28; Mismatches 36; Indels 20; Gaps 4;

```

```

QY 1 QVQLQESGAEIVRSASVNICTASGPNIKDYMMHWKORPEBGLMIGYIDPSGTEY 60
DB 27 QVQLQESGAEIVRSASVNICTASGPNIKDYMMHWKORPEBGLMIGYIDPSGTEY 86
QY 61 APNQGKATVADTSSNTAYLHLSLTSEDTVYVCNAVLYEYDGL-----YALDYWGQ 115
DB 87 APNQGKATVADTSSNTAYLHLSLTSEDTVYVCNAVLYEYDGL-----YALDYWGQ 139
QY 116 TTVVSSGGSGGGSGGGSGGGSDIELTQSPSLAVSAGEKYAMCKSSQSLFNSRTKRY 175
DB 140 TTVVSSGGSGGGSGGGSGGGSENVLTQSPALMGSAPGEKVTITCSASSV-----SY 192
QY 176 LAWYQKRGQSPKLIYASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSY 235
DB 193 MEMFOQKRGTSPKLMTYSTMLASGVPRFSGSGSGTDFLTITSSVOAEDLAVYCKQSY 252
QY 236 NLTP-TFGGSKLEIK 249
DB 253 SYPLTFAGTLEIK 267

```

```

RESULT 7
US-08-860-174A-10
Sequence 10, Application US/08860174A
Patent No. 5898930
GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOOT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.

```

```

STATE: UNITED STATES
COUNTRY: 3918
ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-860-174A-10

```

```

Query Match      66.7%; Score 877.5; DB 2; Length 282;
Best Local Similarity 68.0%; Pred. No. 8.3e-66;
Matches 170; Conservative 20; Mismatches 57; Indels 3; Gaps 3;

```

```

QY 1 QVQLQESGAEIVRSASVNICTASGPNIKDYMMHWKORPEBGLMIGYIDPSGTEY 60
DB 23 QVQLQESGAEIVRSASVNICTASGPNIKDYMMHWKORPEBGLMIGYIDPSGTEY 82
QY 61 APNQGKATVADTSSNTAYLHLSLTSEDTVYVCNAVLYEYDGLDYALDYWGQTTVY 120
DB 83 SDNVKGFPTISRDGNKNTLYLQMSLSKSEDTAYYCARHGYG-KGY-PDYWGQTTVY 140
QY 121 SSGGGSGGGSGGGSGGGSDIELTQSPSLAVSAGEKYAMCKSSQSLFNSRTKRYLA 180
DB 141 SSGGGSGGGSGGGSGGGSDIELTQSPSLAVSAGEKYAMCKSSQSLFNSRTKRYLA 200
QY 181 QKPGQSPKLIYASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSYNP-T 239
DB 201 QKPGQSPKLIYASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSYNP-T 260
QY 240 FGGGSKLEIK 249
DB 261 FGGGSKLEIK 270

```

```

RESULT 8
US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezia Somanadaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

```

RESULT 9  
 US-09-188-082-16  
 Sequence 16, Application US/09188082  
 Patent No. 6270765  
 GENERAL INFORMATION:  
 APPLICANT: Yashwant M. Deo  
 APPLICANT: Joel Goldstein  
 APPLICANT: Robert Graziano  
 APPLICANT: Chetian Somasundaram  
 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISING  
 TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHYE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/188,082  
 FILING DATE:

RESULT 10  
 US-09-364-088-16  
 Sequence 16, Application US/09364088  
 Patent No. 6365161  
 GENERAL INFORMATION:  
 APPLICANT: Yashwant M. Deo, et al.  
 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISE  
 TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHYVE & COCKFIELD, LLP  
 STREET: 28 State Street, 24th Floor  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/364,088  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/188,082  
 FILING DATE: 07-JUNE-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/484,172  
 FILING DATE: 07-JUNE-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Remillard, Jane E.

REGISTRATION NUMBER: 38, 872

REFERENCE/DOCKET NUMBER: MXI-043CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-7414

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-364-088-16

Query Match 66.7%; Score 877; DB 4; Length 553;  
 Best Local Similarity 66.5%; Pred. No. 2,1e-65;  
 Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEYA 61  
 DB 278 IKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEYA 337  
 QY 62 PNFQKATVTDTSNTAYILHLSLTSEDTVYYCNAYIYYEYDG-----YALDYWGQGT 116  
 DB 338 PKFQKATFTDTSNTAYILHLSLTSEDTVYYCNAYIYYEYDG-----YALDYWGQGT 390  
 QY 117 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMCKSSQSLFNSRTRKNYL 176  
 DB 391 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMCKSSQSLFNSRTRKNYL 443  
 QY 177 AMYQKPGQSPKVLVYMASTRSGVPDRFTSGSGTDFTLTISVQAQDLAVYYCKQSYN 236  
 DB 444 HMFQKPGTSPKLVYTSNLAWSGVPARFSGSGTSLTISRMEADAAVYYCQQRSS 503  
 QY 237 LP-TPGGTKLEIK 249  
 DB 504 YPLTFGAGTKLEIK 517

## RESULT 11

US-09-102-716-16

Sequence 16, Application US/09102716

Patent No. 6395272

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein

APPLICANT: Robert Graziano

APPLICANT: Chezhian Somaundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

OF ANTI-FC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE &amp; COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/102,716

FILING DATE: 22-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

## REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-102-716-16

Query Match 66.7%; Score 877; DB 4; Length 553;  
 Best Local Similarity 66.5%; Pred. No. 2,1e-65;  
 Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEYA 61  
 DB 278 IKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEYA 337  
 QY 62 PNFQKATVTDTSNTAYILHLSLTSEDTVYYCNAYIYYEYDG-----YALDYWGQGT 116  
 DB 338 PKFQKATFTDTSNTAYILHLSLTSEDTVYYCNAYIYYEYDG-----YALDYWGQGT 390  
 QY 117 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMCKSSQSLFNSRTRKNYL 176  
 DB 391 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMCKSSQSLFNSRTRKNYL 443  
 QY 177 AMYQKPGQSPKVLVYMASTRSGVPDRFTSGSGTDFTLTISVQAQDLAVYYCKQSYN 236  
 DB 444 HMFQKPGTSPKLVYTSNLAWSGVPARFSGSGTSLTISRMEADAAVYYCQQRSS 503  
 QY 237 LP-TPGGTKLEIK 249  
 DB 504 YPLTFGAGTKLEIK 517

## RESULT 12

US-10-092-246-36

Sequence 36, Application US/10092246

Patent No. 6501314

GENERAL INFORMATION:

APPLICANT: The Minister of National Defence, Government of Canada

APPLICANT: Fulton, R E

APPLICANT: Alvi, Azhar E

APPLICANT: Nagata, Leslie

TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M

FILE REFERENCE: NEU-0007

CURRENT APPLICATION NUMBER: US/10/092,246

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn version 3.1

SEQ ID NO 36

TYPE: PRT

LENGTH: 240

ORGANISM: Mouse hybridoma cell line 1A4A1

US-10-092-246-36

Query Match 64.9%; Score 854; DB 4; Length 240;  
 Best Local Similarity 64.8%; Pred. No. 6,3e-64;  
 Matches 162; Conservative 33; Mismatches 41; Indels 14; Gaps 3;

QY 1 QYKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEY 60  
 DB 3 QYKLOESGAEIVRSASVNLCTASGFNIKDYMHVWKQPREGLWIGYIDPESGETEY 62  
 QY 61 APNFGKATVTDTSNTAYILHLSLTSEDTVYYCNAYIYYEYDGAYADYWGQGTTVTV 120  
 DB 63 SETFGKATLTVDTSSNTAYILHLSLTSEDTVYYCNAYIYYEYDGAYADYWGQGTTVTV 115  
 QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMCKSSQSLFNSRTRKNYLAWQ 180

Db 116 SGGGSGSGGSGGSDILTQSPNSLSTISGRIRITCKASODVTA-----VQWYQ 169  
QY 181 QKPGSPKVLTYMASTRESGVDPDRFTSGSGSTDPFLTITSSVQADIAVYCKOSYNLP-T 239  
Db 170 QRPQSPPLTFWSTNHTGVPDRFTSGSGSTDPFLTITSSVQADIAVYCKOSYNLP-T 229  
QY 240 FGGGTKLEIK 249  
Db 230 FGGGTKLEIK 239

## RESULT 13

US-09-649-063-23  
Sequence 23, Application US/09649063  
Patent No. 6600022  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakui  
USHO, Shimpai  
KUNIKATA, Toshio  
KURIMOTO, Masashi  
TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/649,063  
FILING DATE: 29-Aug-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,140  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 52,526/1997  
FILING DATE: 21-FEB-1997  
APPLICATION NUMBER: JP 163,490/1997  
FILING DATE: 6-JUN-1997  
APPLICATION NUMBER: JP 215,490/1997  
FILING DATE: 28-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-649-063-23

Query Match 64.3%; Score 846; DB 4; Length 248;  
Best local Similarity 63.6%; Pred. No. 3e-63;  
Matches 159; Conservative 37; Mismatches 44; Indels 10; Gaps 3;

QY 1 QVKLQESGAELVIRGASVNLSTASGFNIKDYMHVWKQRPBESLEWIGYIDPESGETEY 60  
Db 1 EVQLQSSGAELVIRGASVNLSTASGFNIKDYMHVWKQRPBESLEWIGYIDPESGETEY 60  
QY 61 APNFGKATVADTSNTAYLHLSTLSEDTLVYVCNAVITYYEDGYALDYWGQGTIVTV 120

Db 61 GPNFQDKATITPDTSSNTAYLQLRSLTSEDTNAVYYCARQNY---GAGFGWGQGTIVTV 117  
QY 121 SGGGSGSGGSGGSGSDILTQSPNSLSTISGRIRITCKASODVTA-----VQWYQ 180  
Db 118 SAGGSGSGGSGGSGSDILTQSPNSLSTISGRIRITCKASODVTA-----VQWYQ 171  
QY 181 QKPGSPKVLTYMASTRESGVDPDRFTSGSGSTDPFLTITSSVQADIAVYCKOSYNLP-T 239  
Db 172 QRPQSPPLTFWSTNHTGVPDRFTSGSGSTDPFLTITSSVQADIAVYCKOSYNLP-T 229  
QY 240 FGGGTKLEIK 249  
Db 232 FGGGTKLEIK 241

## RESULT 14

US-08-797-689-18  
Sequence 18, Application US/08797689  
Patent No. 5876969  
GENERAL INFORMATION:  
APPLICANT: Fleer, Reinhard  
APPLICANT: Fournier, Alain  
APPLICANT: Guitton, Jean-Dominique  
APPLICANT: Jung, Gerard  
APPLICANT: Yeh, Patrice  
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-797-689-18

Query Match 64.1%; Score 842.5; DB 2; Length 249;  
Best local Similarity 64.6%; Pred. No. 6e-63;  
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;

QY 1 QVKLQESGAELVIRGASVNLSTASGFNIKDYMHVWKQRPBESLEWIGYIDPESGETEY 60

```

Db      4 QVQLQSGAEIVKPGASVYKISCKASGYAFSRSMNWVKORPGQGLEWIGRIYFGDGTXY 63
QY      61 AENPQKATVYTDTSNTAYLHLSTLTSDITVYVC---NAVITYEYDVALDYWGQGT 116
Db      64 NGKFKGKATLTDKSSSTAYMQLSLITVGSAYVFAKKNR--FDERGYAMDYWGQGT 121
QY      117 TTVSSGGGGSGGGSGGSDIELTQSPSSLAVSAGEKVAMSCSSQGLFNSRTKNTL 176
Db      122 TTVSSGGGGSGGGSGGGSNLTQSPNSMSTVGDVRSITCKASQDVDTN-----V 175
QY      177 AMYQKPGQSPKVLITWASTRESGVDPDRTGSGSGTDFTLTSSVQAEDLAVYCKQSYN 236
Db      176 AMYQKPGQSPKVLITWASTRHTGVPDRTGSGSGTDFTLTISNVQSEDSADYFCQOYSS 235
QY      237 LP-TFGGGTKLEIK 249
Db      236 YPWTFGGGTKLEIK 249

RESULT 15
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686172
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guilleton, Jean-Dominique
; Jung, Gerard
; Yeh, Patricia
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentln)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

```

US-09-984-186-18
Query Match      64.1%; Score 842.5; DB 4; Length 249;
Best Local Similarity 64.6%; Pred No. 66-63;
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;

QY      1 QVQLQSGAEIVKPGASVYKISCKASGYAFSRSMNWVKORPGRGLEWIGRIYFGDGTXY 60
Db      4 QVQLQSGAEIVKPGASVYKISCKASGYAFSRSMNWVKORPGRGLEWIGRIYFGDGTXY 63
QY      61 AENPQKATVYTDTSNTAYLHLSTLTSDITVYVC---NAVITYEYDVALDYWGQGT 116
Db      64 NGKFKGKATLTDKSSSTAYMQLSLITVGSAYVFAKKNR--FDERGYAMDYWGQGT 121
QY      117 TTVSSGGGGSGGGSGGSDIELTQSPSSLAVSAGEKVAMSCSSQGLFNSRTKNTL 176
Db      122 TTVSSGGGGSGGGSGGGSNLTQSPNSMSTVGDVRSITCKASQDVDTN-----V 175
QY      177 AMYQKPGQSPKVLITWASTRESGVDPDRTGSGSGTDFTLTSSVQAEDLAVYCKQSYN 236
Db      176 AMYQKPGQSPKVLITWASTRHTGVPDRTGSGSGTDFTLTISNVQSEDSADYFCQOYSS 235
QY      237 LP-TFGGGTKLEIK 249
Db      236 YPWTFGGGTKLEIK 249

```

Search completed: July 30, 2004, 11:22:27  
Job time: 15.6768 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:36 ; Search time 13.6646 Seconds  
(without alignments)  
1752.823 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315  
Sequence: 1 QVTLQSGAEIVRSAGSVNL.....YCKQSYNLPFGGTXLEIK 249

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: \*  
1: pirl: \*  
2: pirl2: \*  
3: pirl3: \*  
4: pirl4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	65.2	268	2 A56446	Ig heavy chain V r
2	854.5	65.0	249	2 S41374	single chain Fv an
3	841.5	64.0	233	2 JCS322	p53 specific singl
4	544	40.9	112	2 S43103	Ig kappa chain V-J
5	538	40.5	113	2 PT0407	Ig light chain V r
6	533	40.5	112	2 PL0265	Ig kappa chain V r
7	533	40.5	113	2 PS0023	Ig kappa chain pre
8	520	39.5	113	2 PT0408	Ig light chain V r
9	514	39.1	112	2 S41393	Ig kappa chain V r
10	503.5	38.3	111	2 S03304	Ig kappa chain V r
11	501.5	38.1	136	2 S04576	Ig heavy chain pre
12	498	37.9	104	2 PH1101	Ig light chain V r
13	497	37.8	103	2 PH1047	Ig light chain V r
14	497	37.8	104	2 PH1102	Ig light chain V r
15	492	37.4	103	2 PH1051	Ig light chain V r
16	492	37.4	103	2 PH1052	Ig light chain V r
17	492	37.4	104	2 PH1104	Ig light chain V r
18	491	37.3	103	2 PH1050	Ig light chain V r
19	489.5	37.2	220	2 A31790	Ig kappa chain V r
20	489	37.2	120	2 G33932	Ig kappa chain pre
21	486	37.0	135	2 S38807	Ig light chain V-J
22	486	37.0	178	2 S29594	Ig gamma chain (MM
23	484.5	36.8	113	2 PL0263	Ig kappa chain V r
24	484	36.8	101	2 PH1063	Ig light chain V r
25	484	36.8	104	2 PH1103	Ig light chain V r
26	480	36.5	111	2 G30502	Ig kappa chain V r
27	479	36.4	118	2 PT0356	Ig kappa chain V r
28	478.5	36.4	134	2 PC1214	Ig kappa chain pre
29	477.5	36.3	117	2 S17586	Ig heavy chain V r

30	477.5	36.3	214	2 S69212	Ig kappa chain (Ma
31	475	36.1	138	2 S26040	Ig kappa chain pre
32	474.5	36.1	113	2 PL0264	Ig kappa chain V r
33	474.5	36.1	120	2 S03471	Ig heavy chain V-D
34	470.5	35.8	240	2 S06084	Ig kappa chain pre
35	469	35.7	122	2 S06823	Ig heavy chain V r
36	468.5	35.6	112	2 E30538	Ig kappa chain V r
37	468.5	35.6	112	2 F30538	Ig kappa chain V r
38	468	35.6	116	2 S15672	Ig heavy chain V r
39	467.5	35.6	113	2 UC2270	Ig heavy chain V r
40	467.5	35.6	118	2 S25174	PL7-6 antibody lig
41	467	35.5	121	2 S49220	Ig heavy chain V r
42	466	35.4	112	2 S09970	Ig gamma-1 chain -
43	465	35.4	97	2 A42575	Ig kappa chain V-J
44	464	35.3	133	1 K4HUT	Ig kappa chain V r
45	463.5	35.2	113	2 S30520	Ig kappa chain pre

## ALIGNMENTS

## RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446 R;Yang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.

U. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally den

A/Reference number: A56446; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotrimer; immunoglobulin

Query Match 65.2%; Score 857; DB 2; Length 268;

Best Local Similarity 66.8%; Pred. No. 9.9e-54;

Matches 167; Conservative 26; Mismatches 45; Indels 12; Gaps 3;

QY	1 QVTLQSGAEIVRSAGSVNLCTASGFNFKDYVMHWKORPEGLWIGYIDSEGETVEY 60	
DB	3 QVTLQSGAEIVKPGASVLSCTTSFNIKIDYIMHWKORPEGLWIGRIAPANGITKY 62	
QY	61 ADFPGKATVADTSSNTAYIMLSLTSEDTVYYCNNAVYYEDGVALDYWGQGTIVY 120	
DB	63 DKFPGKATVADTSSNTAYIQLSLTSEDTVYYCASYLFRYE---NYWGQGTIVY 118	
QY	121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKAMCKSSQIFNSRTRKNYLAAYQ 180	
DB	119 SSGGGSGGGSGGGSDIELTQSPALMSASIGEKYTMSCRASSV-----NFTWYQ 171	
QY	181 QKPGSPKVLVMASTRESGVDPDRFTGSSGSDFTLTISVQAEIDIAVYCKQSYNLP-T 239	
DB	172 QSDMSPKMAYVYITSLRPGVARRSGSGSGMSYSLTISMGEADATYYCQGFSSPFT 231	
QY	240 FGGGTXTLEIK 249	
DB	232 FGGGTXTLEIK 241	

## RESULT 2

S41374 single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C/Accession: S41374

R;Ritsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibo





A:Residues: 1-112 <SHL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-96/Domain: immunoglobulin homology <IMM>  
F:24-40/Region: complementarity-determining 1  
F:41-55/Region: framework 2  
F:56-62/Region: complementarity-determining 2  
F:63-94/Region: framework 3  
F:95-102/Region: complementarity-determining 3  
F:103-112/Region: framework 4

Query Match            40.5%;    Score 533;    DB 2;    Length 112;  
Best Local Similarity   92.0%;    Pred. No. 3.3e-31;  
Matches   103;    Conservative   4;    Mismatches   5;    Indels   0;    Gaps   0;

QY         138 DIETQSPSIAVSAEKVMSCSSQSLFNSTRKKNLYAWYQQKPGQSPKLIYMASTR   197  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db         1 DIVMSQSPSLAVASAEKVMSCKSSQSLFNSTRKKNLYAWYQQKPGQSPKLIYMASTR   60  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY         198 ESGVPDRFTGSGSGTDTLTITISSVAEDLAAYYCQSYNLPFTFGGTGLEIK   249  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
        61 ESGVPDRFTGSGSGTDTLTITISSVAEDLAAYYCQSYNLPFTFGGTGLEIK   112  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7  
PS0023  
Ig kappa chain precursor V region (6A4) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PS0023  
R:Margret, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.  
Gene 74, 335-345, 1988  
A>Title: Cloning and characterization of cDNAs coding for the heavy and light chains of A:Reference number: PS0023; MUID:89232725; PMID:3149944  
A:Molecule type: mRNA  
A:Residues: 1-133 <MAR>  
A:Experimental source: strain BALB/c  
A>Note: the amino-terminal four residues of the mature protein were directly sequenced C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>  
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match            40.5%;    Score 533;    DB 2;    Length 133;  
Best Local Similarity   89.7%;    Pred. No. 3.9e-31;  
Matches   104;    Conservative   4;    Mismatches   8;    Indels   0;    Gaps   0;

QY         134 GGGSDELTMQSPSLAVASAEKVMSCKSSQSLFNSTRKKNLYAWYQQKPGQSPKLIYW   193  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db         17 GTGGDVTWMSQSPSLAVASAEKVMSCKSSQSLFNSTRKKNLYAWYQQKPGQSPKLIYW   76  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY         194 ASTRESGVPRFTGSGSGTDTLTITISSVAEDLAAYYCQSYNLPFTFGGTGLEIK   249  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
        77 ASTRESGVPRFTGSGSGTDTLTITISSVAEDLAAYYCQSYNLPFTFGGTGLEIK   132  
          ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8  
PT0408  
Ig light chain V region (SI07/VH1 group 1-6) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PT0408  
J:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A>Title: Characterization of somatically mutated SI07 VH1-encoded anti-DNA autoantibodies A:Reference number: PT0376; MUID:91147903; PMID:1900082  
A:Accession: PT0408  
A:Molecule type: DNA  
A:Residues: 1-113 <BEH>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 520; DB 2; Length 113;  
Best Local Similarity 90.2%; Pred. No. 2,7e-30;  
Matches 101; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 138 DIETQSPSSILAVSAGEKVMSCSKSSQSLFNSRTRKNYLAWYQKFGQSPKLLIYMASTR 197  
||:|||||  
DB 1 DIVMSQSPSSILAVSAGEKVMSCSKSSQSLFNSRTRKNYLAWYQKFGQSPKLLIYMASTR 60

OY 198 ESGVDRRTGSGSGTDFTLTITSSVQAEIDLAVVYCKQSYNLPFTGGGGTKLEIK 249  
||:|||||  
DB 61 ECGVDRRTGSGSGTDFTLTITSSVQAEIDLAVVYCKQSYNLPFTGGGTXLEIK 112

RESULT 9

S41393  
Ig kappa chain V region (12.5H VL) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
C;Accession: S41393  
R;Margarette, C.; Gilbert, D.; Brard, F.; Tron, F.  
Submitted to the EMBL Data Library, January 1994  
A;Description: Structural characterization of an (NZB X NZW) F1 mouse-derived Igm anti-  
A;Reference number: S41393  
A;Accession: S41393  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <MAR>  
A;Cross-References: EMBL:Z29536  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 514; DB 2; Length 112;  
Best Local Similarity 88.4%; Pred. No. 7.2e-30;  
Matches 99; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 138 DIETQSPSSILAVSAGEKVMSCSKSSQSLFNSRTRKNYLAWYQKFGQSPKLLIYMASTR 197  
||:|||||  
DB 1 DIVMSQSPSSILAVSAGEKVMSCSKSSQSLFNSRTRKNYLAWYQKFGQSPKLLIYMASTR 60

OY 198 ESGVDRRTGSGSGTDFTLTITSSVQAEIDLAVVYCKQSYNLPFTGGGGTKLEIK 249  
||:|||||  
DB 61 DSGVDRRTGSGSGTDFTLTITSSVQAEIDLAVVYCKQSYNLPFTGGGGTKLEIK 112

RESULT 10

S03304  
Ig kappa chain V region (61B8) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000  
C;Accession: S03304; UI0043  
R;Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.  
J. Exp. Med. 167, 1841-1848, 1988  
A;Title: Do antibodies recognize amino acid side chains of protein antigens independent  
A;Reference number: JI0043; PMID:88258372; PMID:2455014  
A;Accession: S03304  
A;Molecule type: mRNA  
A;Residues: 1-111 <VAN>  
A;Cross-References: EMBL:X12380; NID:G52341; PIDD:CAA03938.1; PID:G930189  
A;Note: the authors translated the codon GAT for residue 76 as Asn  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 503.5; DB 2; Length 111;  
Best Local Similarity 89.2%; Pred. No. 4e-29;  
Matches 99; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

138 DIETQSPSSILAVSAGEKVMSCSKSSQSLFNSRTRKNYLAWYQKFGQSPKLLIYMASTR 197

Db 1 DIVTSGSPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGGGTKLE 247  
 Db 61 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGGGTKLE 111

## RESULT 11

S04576

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000

C/Accession: S04576

R/Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th

Eur. J. Immunol. 17, 91-95, 1987

A/Title: Molecular analysis of the murine lupus-associated anti-self response: involve

A/Reference number: S04573; MUID:87133856; PMID:3102255

A/Accession: S04576

A/Molecule type: mRNA

A/Residues: 1-136 &lt;KOF&gt;

A/Cross-references: EMBL:X14624; NID:g52029; PID:CAA32777.1; PID:g52030

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F/20-136/Product: Ig heavy chain V region (fragment) #status predicted &lt;MAT&gt;

F/34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 38.1%; Score 501.5; DB 2; Length 136;  
 Best Local Similarity 77.0%; Pred. No. 6.9e-29;

Matches 94; Conservative 11; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVKLESGSEIVRSAGSVNLCTASGFNTKDYMMWVKRPREGLFMIGYIDPESGETRY 60  
 Db 20 EYVLQSGSEIVRPGASVNLCTASGFNTKDYMMWVKRPREGLFMIGYIDPESGETRY 79

QY 61 APNFOGKATVATDTSNTFAVLAHLSITSEDTVYVCNAVITYEYGVALDYWGQGTITV 120  
 Db 80 ASKFGKATVATDTSNTFAVLAHLSITSEDTVYVCNAVITYEYGVALDYWGQGTITV 134

QY 121 SS 122  
 Db 135 SS 136

## RESULT 12

PH1101

Ig light chain V region (clone 111.19) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1101

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1101

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-104 &lt;TIL&gt;

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 37.9%; Score 498; DB 2; Length 104;  
 Best Local Similarity 92.3%; Pred. No. 9e-29;

Matches 96; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELOSPPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 197  
 Db 1 DIVTSGSPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 241

Db 61 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 104

## RESULT 13

PH1047

Ig light chain V region (clones 165.45 and 163.c1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1047; PH1049

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1047

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-103 &lt;TIL&gt;

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 37.8%; Score 497; DB 2; Length 103;  
 Best Local Similarity 93.2%; Pred. No. 1e-28;

Matches 96; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 138 DIELOSPPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 197  
 Db 1 DIVTSGSPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 240  
 Db 61 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 103

## RESULT 14

PH1102

Ig light chain V region (clone 111.61) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: PH1102

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1102

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-104 &lt;TIL&gt;

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 37.8%; Score 497; DB 2; Length 104;  
 Best Local Similarity 91.3%; Pred. No. 1.1e-28;

Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELOSPPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 197  
 Db 1 DIVTSGSPSLAVSAGEKNTLTCKSSQILNSTRTKNTLAWYQKRGSPKLLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 241  
 Db 61 ESGVDPDRFTGSGSGTDFTLTITSSVQAEADLAVYCKOSYNLP-TPGG 104

## RESULT 15

PH1051

Ig light chain V region (clone 165.3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1051  
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH1051  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-103 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:16-96/Domain: immunoglobulin homology <IMM>

Query March 37.4%; Score 492; DB 2; Length 103;  
 Best local similarity 92.2%; Pred. No. 2.4e-28;  
 Matches 95; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 138 DIELTQSPSSLAVSAGEKVMSCSKSSQSLFNSRTKRYLIAMYOQKPGQSEKVIITYMASTR 197  
 Db 1 DIVMSQSPSSLAVSAGEKVMSCSKSSQSLNRRTRKRYLIAMYOQKPGQSPKLIITYMASTR 60  
 QY 198 ESGVPDRFTGSGSGTDFTLTISVQAEELAVYCKQSYNLPTF 240  
 Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEELAVYCKQSYNLPTF 103

Search completed: July 30, 2004, 11:21:46  
 Job time: 13.6646 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model1

Run on: July 30, 2004, 11:55:41 ; Search time 8.09756 Seconds

(without alignments)  
1601.157 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 QVKGQSGAGELVNRGASVNL.....YCKQSYNLPTFGGCTKLEIK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_42:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	464	35.3	133	1 KVA8_HUMAN	P06313 homo sapien
2	463.5	35.2	134	1 KVA4_HUMAN	P06314 homo sapien
3	448.5	34.1	114	1 KVA4_HUMAN	P01625 homo sapien
4	418	31.8	121	1 KVA4_HUMAN	P03593 homo sapien
5	405.5	30.8	109	1 KVA4_HUMAN	P01751 mus musculu
6	400	30.4	139	1 KVA4_HUMAN	P01751 mus musculu
7	393.5	29.9	114	1 KVA4_HUMAN	P01747 mus musculu
8	393.5	29.9	120	1 KVA4_HUMAN	P01633 mus musculu
9	380.5	28.9	149	1 KVA4_HUMAN	P01634 mus musculu
10	378.5	28.8	136	1 KVA4_HUMAN	P01755 mus musculu
11	378	28.7	137	1 KVA4_HUMAN	P01746 mus musculu
12	376.5	28.6	140	1 KVA4_HUMAN	P01745 mus musculu
13	375.5	28.6	121	1 KVA4_HUMAN	P04431 homo sapien
14	371.5	28.3	129	1 KVA4_HUMAN	P01605 homo sapien
15	369.5	28.1	108	1 KVA4_HUMAN	P01600 homo sapien
16	367.5	27.9	108	1 KVA4_HUMAN	P01744 homo sapien
17	366	27.8	147	1 KVA4_HUMAN	P01664 mus musculu
18	365.5	27.8	108	1 KVA4_HUMAN	P01664 mus musculu
19	365.5	27.8	111	1 KVA4_HUMAN	P01622 homo sapien
20	365.5	27.8	117	1 KVA4_HUMAN	P01622 homo sapien
21	363	27.6	109	1 KVA4_HUMAN	P01622 homo sapien
22	362	27.5	129	1 KVA4_HUMAN	P01622 homo sapien
23	361.5	27.5	108	1 KVA4_HUMAN	P01622 homo sapien
24	361.5	27.5	111	1 KVA4_HUMAN	P01622 homo sapien
25	361	27.5	109	1 KVA4_HUMAN	P01622 homo sapien
26	361	27.5	109	1 KVA4_HUMAN	P01622 homo sapien
27	361	27.5	113	1 KVA4_HUMAN	P01622 homo sapien
28	360	27.4	117	1 KVA4_HUMAN	P01622 homo sapien
29	359.5	27.3	117	1 KVA4_HUMAN	P01622 mus musculu
30	359	27.3	120	1 KVA4_HUMAN	P01622 mus musculu
31	358.5	27.3	111	1 KVA4_HUMAN	P04207 homo sapien
32	357	27.1	129	1 KVA4_HUMAN	P01622 mus musculu
33	357	27.1	129	1 KVA4_HUMAN	P01622 mus musculu

34	356.5	27.1	115	1 KVA4_HUMAN	P01614 homo sapien
35	355	27.0	108	1 KVA4_HUMAN	P01619 homo sapien
36	354.5	27.0	111	1 KVA4_HUMAN	P01672 mus musculu
37	354.5	27.0	138	1 KVA4_HUMAN	P03980 mus musculu
38	354	26.9	107	1 KVA4_HUMAN	P01596 mus musculu
39	354	26.9	110	1 KVA4_HUMAN	P01668 mus musculu
40	353.5	26.9	111	1 KVA4_HUMAN	P01671 mus musculu
41	353	26.8	118	1 KVA4_HUMAN	P06330 mus musculu
42	352.5	26.8	108	1 KVA4_HUMAN	P01608 homo sapien
43	352.5	26.8	108	1 KVA4_HUMAN	P01649 mus musculu
44	352.5	26.8	111	1 KVA4_HUMAN	P01667 mus musculu
45	352	26.8	109	1 KVA4_HUMAN	P01623 homo sapien

## ALIGNMENTS

```

RESULT 1
KVAB_HUMAN          STANDARD;          PRT;          133 AA.
ID      KVAB_HUMAN
AC      P06313:
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-IV region JI precursor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86041853; PubMed=2997712;
RA      Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA      Zachau H.G.;
RT      "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT      single germline gene.";
RL      Nucleic Acids Res. 13:615-6529(1985).
CC      -----
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CC      -----
DR      EMBL; Z00022; CA77317.1; -.
DR      PIR; A01904; K4HUT1.
DR      HSSP; P80362; 1WT1.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; P:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; IG_V.
DR      InterPro; IPR003596; IG_Like.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV_1.
DR      PROSITE; PS00835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL          1..20
FT      CHAIN           1..133
FT      DOMAIN          21..43
FT      DOMAIN          44..60
FT      DOMAIN          61..75
FT      DOMAIN          76..82
FT      DOMAIN          83..114
FT      DOMAIN          115..122
FT      DISULFID        43..114
FT      NON_TER         133
SQ      SEQUENCE      133 AA; 14632 MW; 5FB3953066744AF4 CRC64;
Query Match          35.3%; Score 464; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 4e-28;

```

Matches 87; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAMVQKPGSPKLLIYW 193  
 DB 17 GAYGDIWMTQSPDLSIAVSGERATINCKSSQSLVSNKNTLYAMVQKPGSPKLLIYW 76

QY 194 ASTRESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 249  
 DB 77 ASTRESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 132

RESULT 2  
 KY4C\_HUMAN STANDARD; PRT; 134 AA.  
 AC P06314;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-IV region B17 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041854; PubMed=2997713;  
 RA Marsh P., Mills F., Gould H.;  
 RT "Detection of a unique human V kappa IV germline gene by a cloned  
 RT cDNA probe.";  
 RL Nucleic Acids Res. 13:6531-6544 (1985).  
 RN [2]  
 REVISION TO 76.  
 RA Marsh P.;  
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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 CC -----  
 DR EMBL; X02990; CAA26733.1; -  
 DR HSSP; P80362; 1MTL.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Igv\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 KW SIGNAL  
 FT 1 20  
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 61 75 FRAMEWORK-2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 122 133 FRAMEWORK-4.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON\_TER 134 134  
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 35.2%; Score 463.5; DB 1; Length 134;  
 Best Local Similarity 76.1%; Pred. No. 4.4e-28;  
 Matches 89; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAMVQKPGSPKLLIYW 193  
 DB 17 GAYGDIWMTQSPDLSIAVSGERATINCKSSQSLVSNKNTLYAMVQKPGSPKLLIYW 76

DB 17 GAYGDIWMTQSPDLSIAVSGERATINCKSSQSLVSNKNTLYAMVQKPGSPKLLIYW 76

QY 194 ASTRESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 249  
 DB 77 ASTRESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 133

RESULT 3  
 KY4A\_HUMAN STANDARD; PRT; 114 AA.  
 AC P01625;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-IV region Len.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RP SEQUENCE.  
 RX MEDLINE=76004342; PubMed=50995;  
 RA Schneider M., Hilschmann N.;  
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
 RN [1]  
 REVISION TO 9.  
 RA Salomon A.;  
 RL Submitted (AUG-1986) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 DR PDB; 1BEQ; 01-FEB-01.  
 DR PDB; 1BEU; 03-FEB-01.  
 DR PDB; 1BEQ; 09-FEB-01.  
 DR PDB; 1EK3; 06-MAR-01.  
 DR PDB; 1LYE; 21-JAN-98.  
 DR PDB; 3LYE; 18-MAY-99.  
 DR PDB; 5LYE; 28-MAR-01.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; Igv\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 41 55 FRAMEWORK-2.  
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 63 94 FRAMEWORK-3.  
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 113 FRAMEWORK-4.  
 FT DISULFID 23 94 BY SIMILARITY.  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 34.1%; Score 448.5; DB 1; Length 114;  
 Best Local Similarity 76.1%; Pred. No. 4.8e-27;  
 Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 138 DIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAMVQKPGSPKLLIYW 197  
 DB 1 DIVMTQSPDLSIAVSGERATINCKSSQSLVSNKNTLYAMVQKPGSPKLLIYW 60

QY 198 ESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 249  
 DB 61 ESGVDRPFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNLPTRGGGTLEIK 113

RESULT 4

KV40 HUMAN STANDARD; PRT; 121 AA.  
 ID KV40 HUMAN  
 AC P06312;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ig kappa chain V-IV region precursor (Fragment).  
 GN IGKV4-1.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=66041853; PubMed=2997712;  
 RA Klobbeck H.G., Bornkamm G.W., Combiato G., Mochkat R., Pohlenz H.D.,  
 RA Zachau H.G.;  
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a  
 RT single germline gene."  
 RL Nucleic Acids Res. 13:6515-6529(1985).  
 CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.  
 CC -----  
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 CC -----  
 DR EMBL; Z00023; CAA7318.1; -;  
 DR PIR; A01902; K4HU.  
 DR HSSP; P80362; 1WTL.  
 DR Genew; HSC5834; IGKV4-1.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 61 75 FRAMEWORK-2.  
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 83 114 FRAMEWORK-3.  
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 43 114 BY SIMILARITY.  
 FT NON\_TER 121 121  
 SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;  
 Query Match 31.8%; Score 418; DB 1; Length 121;  
 Best Local Similarity 74.3%; Pred. No. 9.6e-25;  
 Matches 78; Conservative 11; Mismatches 16; Indels 0; Gaps 0;  
 QY 134 GGGSDIEITQSPSSIAVNAAGEKVMSCSSQSLFNSRRKNTLYAYQQKPGGSPKVLTYW 193  
 DB 17 GAYGIVMTQSPDLSAVLSGERATINCKSSQSVLVSSNNKNLYAYQQKPGGSPKVLTYW 76  
 QY 194 ASTRESGVDPDRFTGSGSGTDFLTITSSVOAEDVAYYCKQSNLP 238  
 DB 77 ASTRESGVDPDRFTGSGSGTDFLTITSSVOAEDVAYYCKQSNLP 121  
 RESULT 5  
 ID KV4D HUMAN STANDARD; PRT; 109 AA.  
 AC P83593;  
 DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-IV region STR (Fragment).  
 GN Ig kappa chain V-IV region STR (Fragment).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Abdominal adipose tissue;  
 RX MEDLINE=98249779; PubMed=9588180.  
 RA Olsen K.E., Sletten K., Westermarck P.;  
 RT "Extended analysis of AL-amyloid protein from abdominal wall  
 RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain."  
 RL Biochem. Biophys. Res. Commun. 245:713-716(1998).  
 CC -1- FUNCTION: May play an important role in fibrillogenesis.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00409; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 41 55 FRAMEWORK-2.  
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 63 94 FRAMEWORK-3.  
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 109 FRAMEWORK-4.  
 FT DISULFID 23 94 BY SIMILARITY.  
 FT UNSURE 23 23  
 FT UNSURE 94 94  
 FT NON\_TER 109 109  
 SQ SEQUENCE 109 AA; 12060 MW; 0CAF31E11E12A0B CRC64;  
 Query Match 30.8%; Score 405.5; DB 1; Length 109;  
 Best Local Similarity 69.7%; Pred. No. 7.3e-24;  
 Matches 76; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 QY 138 DIEITQSPSSIAVNAAGEKVMSCSSQSLFNSRRKNTLYAYQQKPGGSPKVLTYW 197  
 DB 1 DIWVTQSPDLSAVLSGERATINCKSSQSVLVSSNNKNLYAYQQKPGGSPKVLTYW 60  
 QY 198 ESGVDPDRFTGSGSGTDFLTITSSVOAEDVAYYCKQSNLP-TFGGSK 245  
 DB 61 ESGVDPDRFTGSGSGTDFLTITSSVOAEDVAYYCKQSNLP-TFGGSK 109  
 RESULT 6  
 ID HV07 MOUSE STANDARD; PRT; 139 AA.  
 AC P01751; P01752;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region B1-8/186-2 precursor.  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Botwell A.L.M., Paekind M., Reth M., Tanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NpB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL

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CC (NPR ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -.
CC DR PIR; A90809; MEMS18.
CC DR PDB; 1A6U; 27-MAY-98.
CC DR PDB; 1A6W; 15-JUL-98.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region; Signal; 3D-structure.
CC FT SIGNAL 1 19
CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 124 D SEGMENT.
CC FT DOMAIN 125 139 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON TER 139 139
CC SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 30.4%; Score 400; DB 1; Length 139;
Best Local Similarity 63.4%; Pred. No. 2.5e-23;
Matches 78; Conservative 14; Mismatches 27; Indels 4; Gaps 2;

QY 1 QVKGQSGAEIVRSAGSVNLSTAGSFNFKDYVMWVKRPBEGLEWIGYIDPESERTY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVLOQDPGAEIVKPGASVNLSTAGSYFTSYMMHWKQRPGRGLEWIGRIDPNSGGTY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AHNFGKATVATDTSSTNTAYLHLSITSEDTVYVCNAVITYEYDGYA-LDYWGQGTWV 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NKKFKSKATLVYDKRSSTAYMQLSSTSDSAVYTC--ARDYVGSSTFDYWGQGTIT 136
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 VSS 122
   |||
Db 137 VSS 139
   |||

RESULT 7
KVIA_MOUSE STANDARD; PRT; 114 AA.
ID KVIA_MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6788890; Leder P., Scharff M.D.;
RA Kwan S.-P., Radikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains";
RL J. Exp. Med. 153:1366-1370(1981).

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CC -----
CC EMBL; U29423; AAC00033.1; -.
CC DR PIR; A01915; KMS7A.
CC DR HSSP; P01607; IRE1.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region.
CC FT DOMAIN 1 23
CC FT DOMAIN 24 40 FRAMEWORK-1.
CC FT DOMAIN 41 55 FRAMEWORK-2.
CC FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 63 94 FRAMEWORK-3.
CC FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 104 113 FRAMEWORK-4.
CC FT DISULFID 23 94 BY SIMILARITY.
CC FT NON TER 114 114
CC SQ SEQUENCE 114 AA; 12717 MW; 32008BC89DB367B CRC64;

Query Match 29.9%; Score 393.5; DB 1; Length 114;
Best Local Similarity 68.1%; Pred. No. 6e-23;
Matches 77; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 138 DIETQSPSPSLAVSGEKVMSCKSSQSLFNRGTRKNVYAVQKPGGSPKLYWASNR 197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DVTWQSPFTFLAVTASKKTITSTASSTSYSSKSHVHTIAYQKPEQSPKLTIGASNR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 198 ESGVDPDRFTGSGSGDTFTLTITSSVQADPLAVYYCKQSYNLP-TFGGCTGLI 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YGVVDRFTGSGSGDTFTLTITSSVQVDELTHYYCAQFPYSPLTFAGGTGLI 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT. JH2.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region; Hydrindoma.
CC FT DOMAIN 1 111 IG-LIKE.
CC FT NON TER 120 120
CC SQ SEQUENCE 120 AA; 13307 MW; PF04FA4A167B654AF CRC64;

```



Query Match 29.9%; Score 393.5; DB 1; Length 120;  
 Best Local Similarity 60.3%; Pred. No. 6.4e-23;  
 Matches 73; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 2 VKLQESGAEIVRSASVNLSTAGSEINIKQYMMWVQREBEGLWIGYIDPESGETEYA 61  
 Db 1 VOLOQSGAEIVRSASVNLSTAGSEINIKQYMMWVQREBEGLWIGYIDPESGETEYA 60  
 QY 62 PNFQKATVTADTSSNTAYLHLSLTSEDTVVYCNNAVYEXDYALDYWGQGTVTYS 121  
 Db 61 EKKFGKTTTLTVDKSSSTAYVQLRSTSEDSAVYFCASVYTG-GSYTFDYWGQGTTLTVS 119  
 QY 122 S 122  
 Db 120 S 120

RESULT 9  
 KVS5\_MOUSE STANDARD; PRT; 149 AA.  
 AC P01633;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region MFC11 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE OF 1-71 FROM N.A.  
 RX MEDLINE=83001944; PubMed=6288267;  
 RA Kelley D.B., Coleclough C., Perry R.P.;  
 RT "Functional significance and evolutionary development of the  
 RT 5'-terminal regions of immunoglobulin variable-region genes.";  
 RL Cell 29:681-689(1982).  
 RN [2]  
 RP SEQUENCE OF 41-149 FROM N.A.  
 RX MEDLINE=80176554; PubMed=6245773;  
 RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;  
 RT "The variability, arrangement, and rearrangement of immunoglobulin  
 RT genes";  
 RL Can. J. Biochem. 58:176-187(1980).  
 RN [3]  
 RP SEQUENCE OF 30-149.  
 RX MEDLINE=78186617; PubMed=418775;  
 RA Smith G.P.;  
 RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
 RT myeloma MPC 11.";  
 RL Biochem. J. 171:337-347(1978).  
 RL -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS  
 CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE  
 CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL  
 CC RESIDUE OF TYPICAL KAPPA CHAINS.  
 CC -----  
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 CC -----  
 CC EMBL; J00561; AAA38776.1; -  
 DR PIR; A90823; KVM511.  
 DR HSSP; P80362; IWT1.  
 DR InterPro; IPR007110; Ig\_1like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Signal; Repeat.

FT SIGNAL 1 29  
 FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MFC11.  
 FT DOMAIN 42 64 FRAMEWORK-1.  
 FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 76 90 FRAMEWORK-2.  
 FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 98 129 FRAMEWORK-3.  
 FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 139 148 FRAMEWORK-4.  
 FT REPEAT 26 35  
 FT REPEAT 38 47  
 FT NON TER 149 149  
 SQ SEQUENCE 149 AA; 16434 MM; B0480C87B682AC3E CRC64;

Query Match 28.9%; Score 380.5; DB 1; Length 149;  
 Best Local Similarity 65.0%; Pred. No. 7.6e-22;  
 Matches 76; Conservative 16; Mismatches 18; Indels 7; Gaps 2;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCSKSOSLFNSRTKNTLAMYQKPGSPKTLITW 193  
 Db 38 GVDGDIWMTQSHKFMSTSVGDRVSTCKASQDVSTT-----VAMYQKPGSPKTLITW 91  
 QY 194 ASTRESGVDPDRFTGSGSGTDFTLTSSVQAEPLAVYCKQSYNL-PTFGGTRKLETK 249  
 Db 92 ASYRTYGVDRFTGSGSGTDFTLTSSVQAEPLAVYCKQHYSTPPTFGGTRKLETK 148

RESULT 10  
 KVS5\_MOUSE STANDARD; PRT; 136 AA.  
 AC P01634;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig kappa chain V-V region MOPC 21 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82059477; PubMed=6170937;  
 RA Hamlyn P.H., Galt M.J., Milstein C.;  
 RT "Complete sequence of an immunoglobulin mRNA using specific priming  
 RT and the dideoxynucleotide method of RNA sequencing.";  
 RL Nucleic Acids Res. 9:4485-4494(1981).  
 RN [2]  
 RP SEQUENCE OF 30-136.  
 RX MEDLINE=73053310; PubMed=4638343;  
 RA Svasti J., Milstein C.;  
 RT "The complete amino acid sequence of a mouse kappa light chain.";  
 RL Biochem. J. 128:427-444(1972).  
 RL -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS  
 CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE  
 CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL  
 CC RESIDUE OF TYPICAL KAPPA CHAINS.  
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 CC -----  
 CC EMBL; V00810; CAA24192.1; ALU\_TERM.  
 DR PIR; A93736; KVM521.  
 DR PDB; 1IGC; 03-JUN-95.  
 DR InterPro; IPR007110; Ig\_1like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Signal; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.  
 FT DOMAIN 30 52 FRAMEWORK-1.

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FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 64 78 FRAMEWORK-2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 136 FRAMEWORK-4.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996DIC2 CRC64;

Query Match 28.8%; Score 378.5; DB 1; Length 136;
Best Local Similarity 63.2%; Pred. No. 9,6e-22;
Matches 74; Conservative 18; Mismatches 18; Indels 7; Gaps 2;

QY 134 GGGSDIEITQSPSSLAWSAGEKVMKSCSKSGSLFNSRFRKRYLAMYQQKPGQSPVLLIY 193
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB GADGNIVMTQSPKSMMSVGERVLTLCASENVV-----TVSWYQKPEQSPKLLIYG 79
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 194 ASTRESGVDPRTGGSGGTDFLLTSSVQAEFLAYVYCKOSYNDL-TEGGGKLEIK 249
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 80 ASNRYTGVDPRTGGSGATDFLLTSSVQAEFLADYHCGQGYSPYTRGGGKLEIK 136
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
HVI1_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 843 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; GZMS43.
DR HSP; P01810; 2PB1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION 843.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 FRAMEWORK-4.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.

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FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881B44B8E9 CRC64;

Query Match 28.7%; Score 378; DB 1; Length 137;
Best Local Similarity 61.5%; Pred. No. 1.1e-21;
Matches 75; Conservative 11; Mismatches 32; Indels 4; Gaps 2;

QY 1 QVKLOESGAEIVRSQASVNLSCITASGFNIKDYHMYWVQKPEEGLEMTGYIDPESGETEY 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 20 QVQLQGPAAEFVFKGASVYKSCASGYFTSYLMHWVWQKRGLEWIGRIDPNSGGTTY 79
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 APNFGKATVTADTSSNTAYHLHSITSEDTYYCNAVVIYEDYGLADYWGQGTYYTV 120
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 80 NEHFRSKATLTIIDPSSYAWQSLTSEDSAVYVC--ARRLGRY-FDYWGQGTITLV 135
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 121 SS 122
DB 136 SS 137

RESULT 12
HVO2_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Stess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVM5G7.
DR HSP; P01810; 2PB1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5C88 CRC64;

Query Match 28.6%; Score 376.5; DB 1; Length 140;
Best Local Similarity 58.2%; Pred. No. 1.4e-21;
Matches 71; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

QY 1 QVKLOESGAEIVRSQASVNLSCITASGFNIKDYHMYWVQKPEEGLEMTGYIDPESGETEY 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 20 QVQLQGPAAEFVRSQASVYKSCASGYFTSYGINWVWQKRGLEWIGRIDPNSGGTY 79
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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QY 61 APNFGKATVADTSSNTAYLHLSLTSEDTVVYCNAYIYEXDGYALDYMGGTIVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKKKGTITLVDDSSSTAYWQRLSTSEDAVYFCARSHYGG-GSYDFYWGQGTITLV 138

QY 121 SS 122
   ||
Db 139 SS 140

RESULT 13
HVO1_MOUSE STANDARD; PRT; 121 AA.
ID HVO1_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region Mpc 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
   region of immunoglobulin heavy chain Mpc11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCALANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
   FROM A MELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A93708; GWSM11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 28.6%; Score 375.5; DB 1; Length 121;
Best Local Similarity 59.0%; Pred. No. 1.4e-21;
Matches 72; Conservative 18; Mismatches 31; Indels 1; Gaps 1;

QY 1 QVKIQSGAEIVRSQASVNLSTASGPNIKDYVMHWYKOREEGLEWIGYIDPSGETEY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EAOLQOSGAELVRPGTSVKISCKAAGYFTFYWGWERGHHGIEWGIDYIPGSGFTNY 60

QY 61 APNFGKATVADTSSNTAYLHLSLTSEDTVVYCNAYIYEXDGYALDYMGGTIVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NDNLKGRATLTADTSSSTAYLQLSSLTSEDAIYFCARGIYNSPY-FDSWGQGTITLV 119

QY 121 SS 122
   ||
Db 120 SS 121

RESULT 14
KVIM_HUMAN STANDARD; PRT; 129 AA.
ID KVIM_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=85014149; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
   lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; GAA25477.1; ALT_TERM.
DR PIR; A01883; K1HWK.
DR HSSP; P01607; IRET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 46 56 FRAMEWORK-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 111 119 FRAMEWORK-3.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match 28.3%; Score 371.5; DB 1; Length 129;
Best Local Similarity 62.4%; Pred. No. 3e-21;
Matches 73; Conservative 20; Mismatches 17; Indels 7; Gaps 2;

QY 134 GGSGLDILTPSSSLAVSAGEKYAMSCSSQSLFNSRTRKNYLYAMYOQKPGOSPVLITYW 193
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 GARDICQMTQSPSSLSASVSGDRVITTCRASGI-----SYLAWMYQKPKAKPRLIYA 72

QY 194 ASTRESGVDPRTFGSGSGTDFTLTISSVQAEIDLAVYCKQSYN-LPTFGGCTKLEIK 249
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 ASHSQGVTSRFSGSGGTDFTLTISLQPEDSATYVCOQSYSTLTITGGQTRLEIK 129

RESULT 15
KVIM_HUMAN STANDARD; PRT; 108 AA.
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=77038198; PubMed=824717;

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RA  Capra J.D., Klapper D.G.;
RT  "Complete amino acid sequence of the variable domains of two human
RT  IgM anti-gamma globulins (Iay/Pom) with shared idiotypic
RT  specificities."
RL  Scand. J. Immunol. 5:677-684(1976).
CC  -1- MISCELLANEOUS; THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC  CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC  WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC  -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC  GLOBULIN ACTIVITY.
DR  PIR; A01871; K1HOLY.
DR  HSSP; P01607; 1REI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; IG-like.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 FRAMEWORK-1.
FT  DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 35 49 FRAMEWORK-2.
FT  DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 57 88 FRAMEWORK-3.
FT  DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 98 107 FRAMEWORK-4.
FT  DISULFID 23 88 BY SIMILARITY.
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 28.1%; Score 369.5; DB 1; Length 108;
Best Local Similarity 62.8%; Pred. No. 3.5e-21;
Matches 71; Conservative 20; Mismatches 15; Indels 7; Gaps 2;

QY 138 DIELTQSSPSLAVSAGEKVAWSCSSOSTLERNRKNYLAAYQOKPGQSPKLIYMASTR 197
DB 1 DIQMTQSSPSLAVSYGDRYTTTCNSQNV-----NATLAWYQOKPGLAFLKLIYGASTR 54
QY 198 ESGVDRFTGSGSGTDFLTITSSVQAEIDLAVYCKOSYNL-PTFGGTRLEIK 249
DB 55 EAGVSRFRSGSGSGTDFTTTSSLQPEDIAFYCCQYNNWPPPTFGGTRKVEVK 107

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Search completed: July 30, 2004, 11:19:47  
 Job time : 9.09756 secs



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QY 181 QKPGSPKVLVYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLPF 240
DB 169 QKPGVAPRLTISGATSLTGVPSRPSGSGKDYLTSLTQTEADVATYCCQVWSTPFF 228
QY 241 GGGTGTLEIK 249
DB 229 GGGTGTLEIK 237

RESULT 2
QOYF00 PRELIMINARY; PRT; 298 AA.
AC QOYF00;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAAB8633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 56.6%; Score 744.5; DB 11; Length 298;
Best Local Similarity 56.4%; Pred. No. 1.2e-52;
Matches 141; Conservative 37; Mismatches 61; Indels 11; Gaps 3;

QY 1 QVKLQESGAEIVRSASVNLSTASGFNIKDYMHMVQRPBEGLEWIGYIDPESGETEY 60
DB 40 QVKLQSGSGGLVYKPGSLKLTSCAASGDFSRVMSWVQAPGKGLWIGELNPDSSTINY 99
QY 61 APNPGKATVTADTSSNTAYVHLSLTSEDTTVYVCNAVITYEYGYALDWGGSTVTV 120
DB 100 TPLSLDKRTTISRDNKNTLYLQMSKVRSEDTALYYCARASYGHSA---YWGQGTIVTV 155
QY 121 SSGGGSGGGSGGGSGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRRTKXNYAWQ 180
DB 156 SSGGGSGGGSGGGSGSDIELTQSPSSLASASVGEIVTITTCASGNI-----HNYLAWQ 209
QY 181 QKPGSPKVLVYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYNLP-T 239
DB 210 QKQKSPQLLVYNAKTLADGVPSRPSGSGSTQYSLKINSLPEDFPGSYCOHFWTPTPYT 269
QY 240 FGGGTGTLEIK 249
DB 270 FGGGTGTLEIK 279

RESULT 3
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

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DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.-J., Kim I.-J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 54.2%; Score 713; DB 11; Length 241;
Best Local Similarity 53.8%; Pred. No. 3.3e-50;
Matches 136; Conservative 44; Mismatches 55; Indels 18; Gaps 4;

QY 1 QVKLQESGAEIVRSASVNLSTASGFNIKDYMHMVQRPBEGLEWIGYIDPESGETEY 60
DB 1 QVKLQSGPELKKGETYKISCKASGYFTFDYGMNWWQAGKGLKMGWINTYTGEPY 60
QY 61 APNPGKATVTADTSSNTAYVHLSLTSEDTTVYVCNAVITYEYDGYALDWGGSTVTV 120
DB 61 ADDEKGRAPFSLFMSASTAYVQINNKKEDTATYFCARKDLRY---FDYWGQGTIVTV 116
QY 121 SSGGGSGGGSGGGSGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRRTKXNYAWQ 180
DB 117 SSGGGSGGGSGGGSGSDIELTQSPSSLASLGGGVTTITTCASQDI-----NKLIAYQ 170
QY 181 QKPGSPK---VLVYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAVYCKQSYN 236
DB 171 HKPGKSPSAAITLHY----IQPGLPSRPSGSGSDYSPSISNLPEDDIATYICLHND 226
QY 237 LPTFGGTGTLEIK 249
DB 227 LPTFGGTGTLEIK 239

RESULT 4
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
[2]

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RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
RT of the irradiated mice by treatment with the intestinal RNA of  
RT the same strain."  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK4733.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG LIKE; 1.  
FT NON TER 218 218  
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

[illegible]

RESULT 5			
099L31			
ID	099L31	PRELIMINARY;	PRT; 468 AA.
AC	099L31.		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Similar to RIKEN CDNA 181060009 gene.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Strausberg R.;		
RL	Submitted (FEH-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC003878; AAH03878.1; -.		
DR	PDB; 2AP2; 24-NOV-99.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; Ig; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_MHC; 1.		
DR	PROSITE; PS00290; IG_LIKE; 4.		
DR	SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;		

Query Match	37.5%;	Score 493;	DB 11;	Length 468;
Best Local Similarity	44.9%;	Pred. No. 6.3e-32;		
Matches 118;	Conservative 27;	Mismatches 56;	Indels 62;	Gaps 9

[illegible]

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Db      80  A P K F O D K A T I T T A D T S N T A Y L Q L S L T S E D T A I Y C A R N L L - Y G G - Y D Y M Q G A T T I T V 136
QY      121  S S G G S G S G G G S G S D I E L T Q P S S L A V - - - - - S A G E X A M S C K S Q S L F N S R P R K N 174
Db      137  S S A - - - - - K T T A S V Y P L A P V C G P T T S S Y L G C - - - - - I V K G 169
QY      175  Y L A W Y Q K R G S P K V L I Y A S T R E S G V - - - - - P D R F T G S G S G T D F L T I S V Q A E D L 226
Db      170  Y F - - - - - P E P V T L T M N G S L S G S G V H T E P A V L O S D L Y L S S - - - V I T S S T W P S Q S I 218
QY      227  A V Y Y C K O S Y N L P T F G G G T K L E I K 249
Db      219  - - - - - T O N V A H P A S S T Y V D K K 234

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ID	Q925S2	PRELIMINARY;	PRT;	170 AA.
AC	Q925S2;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	MRP4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c.			
RC	PubMed=11819679;			
RA	Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,			
RA	Su C.;			
RT	"Mechanism of exogenous nucleic acids and their precursors improving			
RT	the repair of intestinal epithelium after irradiation in mice.";			
RL	World J. Gastroenterol. 6:709-717(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c.			
RA	Cui D., Zeng G., Yan X., Li X., Su C.;			
RT	"Cloning of mouse genes related to repairing of intestinal epithelium			
RT	of the irradiated mice by treatment with the intestinal RNA of mice of			
RT	the same strain.";			
RL	Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).			
DR	EMBL; AF240167; AAK3732.1;			
DR	InterPro; IPR007110; IG-1like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
SO	SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;			

Query Match	33.5%;	Score 441;	DB 11;	length 170;
Best Local Similarity	58.6%;	Pred. No. 3e-28;		
Matches	85;	Conservative	15;	Mismatches 41;
				Indels 4;
				Gaps 2;

[illegible]

RESULT 7  
Q9ERZ9  
ID Q9ERZ9 PRELIMINARY; PRT; 107 AA

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AC Q9ER29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-TNF-a monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody."
RL T1 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF262753; AAC23804.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 33.2%; Score 436.5; DB 11; Length 107;
Best Local Similarity 77.6%; Pred. No. 3.9e-28;
Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 141 LTGSPSSIAVAGKGVAMSCSSQSLSLPSRFRKYVLMYQOKPGQSPKVLITYMASTPESG 200
DB 1 MTGSPSSIAVAGKGVAMSCSSQSLSLPSRFRKYVLMYQOKPGQSPKVLITYMASTPESG 60

QY 201 VPDRTSGSGCTDEFTLTITSSVQADLAVYYCKQSGYNLP-ITFGGCTKL 246
DB 61 VPDRTSGSGCTDEFTLTITSSVQADLAVYYCKQSGYNLP-ITFGGCTKL 107

RESULT 8
Q9JL85 PRELIMINARY; PRT; 109 AA.
ID Q9JL85;
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BAJB/c;
RC MEDLINE=20448942; PubMed=1092488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RL with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
EMBL; AF206021; AAF69319.1; -.

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DR HSP: P01810; 2FBT.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CD4DE CRC64;

Query Match 33.0%; Score 433.5; DB 11; Length 109;
Best Local Similarity 70.9%; Pred. No. 6.9e-28;
Matches 83; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 9 AELVRCASVNLCTASGFNIKQYHWVYQREBGLGEMIGYIDPESGTEVYAPNPGKA 68
DB 1 AELVRCASVNLCTASGFNIKQYHWVYQREBGLGEMIGYIDPAGHSHKYPGKA 60

QY 69 TWTADTSSNTAVYHLSTLSEDTTVYYC--NNAVYYEYDGYALDYGQGTVTSS 122
DB 61 TITSDTSSNTAVYQLSSTLSEDTAVYYCYRGAVF-----DYGQGTALTSS 109

RESULT 9
Q924Q3 PRELIMINARY; PRT; 146 AA.
ID Q924Q3;
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AB067797; BAB63282.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1

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PT  NON TER      146      146
SQ  SEQUENCE     146 AA; 16136 MM; CEABDD6E1955807F CRC64;

Query Match
Best Local Similarity 32.0%; Score 420.5; DB 11; Length 146;
Matches 80; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY  1 QVKLOESGALIVRSAGSVNLSCITASGFNIKDYMHVWKQRPBEGLEWIGYIDPESGETEY 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  1 QVQLQPGALIVKPGASVKLSCKASGYTFSTYMMHWKQRPGRGLEWIGRIDNSGGTKY 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  61 APNFGKATVYADTSSNTAYLHLISLTSEDTTYVCNAVYYEYDGYALDYWGQGTIVY 120
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  61 NEKFQKATLTVDKPSSATYMWQLSLTSDSAVYVC-ARSLYDYGDIYAMDYWGQGTISVTV 119
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  121 SS 122
    |||
Db  120 SS 121

RESULT 10
Q924R4 PRELIMINARY; PRT; 145 AA.
ID Q924R4;
AC Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL6.2-D-U-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -.
DR PIR; F28833; F28833.
DR PIR; F39932; F39932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
PT NON TER      145      145
SQ SEQUENCE     145 AA; 16081 MM; ECD0A135B05B8AA CRC64;

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Query Match
Best Local Similarity 31.6%; Score 416; DB 11; Length 145;
Matches 81; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

QY  1 QVKLOESGALIVRSAGSVNLSCITASGFNIKDYMHVWKQRPBEGLEWIGYIDPESGETEY 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  1 QVQLQPGALIVKPGASVKLSCKASGYTFSTYMMHWKQRPGRGLEWIGRIDNSGGTKY 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  61 APNFGKATVYADTSSNTAYLHLISLTSEDTTYVCNAVYYEYDGYALDYWGQGTIVY 120
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  61 NEKFQKATLTVDKPSSATYMWQLSLTSDSAVYVC-ARSDYD-YAMDYWGQGTISVTV 118
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  121 SS 122
    |||
Db  119 SS 120

RESULT 11
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25;
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IGMHC; 1.
SQ SEQUENCE     473 AA; 52449 MM; BE9889B7986DA155 CRC64;

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Query Match
Best Local Similarity 31.5%; Score 414.5; DB 11; Length 473;
Matches 101; Conservative 35; Mismatches 68; Indels 61; Gaps 8;

QY  1 QVKLOESGALIVRSAGSVNLSCITASGFNIKDYMHVWKQRPBEGLEWIGYIDPESGETEY 60
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  20 QVQLQPGALIVKPGASVKLSCKASGYTFTHHTLHWKQRPBEGLEWIGYIPRDGSITKY 79
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  61 APNFGKATVYADTSSNTAYLHLISLTSEDTTYVCNAVYYEYDGYALDYWGQGTIVY 118
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  80 NEKFQKATLTVADKSSSTAYVQNLSTLSDSAVCFRCRGSITTYGYIDYDYGQGTIT 139
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  119 TVSSGGGSGGGSGGGSGGSDITLQSPSSLAV-----SAGEKYAMCKSSQS::FNSKTR 172
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  140 TVSSA-----KTTAPSYVPLAPVCGDTTSSVTLGC-----LV 172
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  173 KNYLAWYQKPGQSPKYLITWASTRESGV-----PDRFTGSGSGTDFTLTSSVQAE 224
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  173 KGYF-----PEPTLLTMSGSLSSGVTFPAVLQSDLYTLSSS---VTVTSSTWESQ 221
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY  225 DIAVYCKQSYNLPFGGQTKLBIX 249
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  222 SI-----TCNVAPPASSTKVDK 239
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
Q924R1 PRELIMINARY; PRT; 145 AA.
ID Q924R1;
AC Q924R1;

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DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB V0186.2-D-J-C-mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067789; BAB63274.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 145
FT SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;
SQ

Query Match 31.3%; Score 412; DB 11; Length 145;
Best Local Similarity 64.0%; Pred. No. 5.6e-26;
Matches 80; Conservative 13; Mismatches 24; Indels 8; Gaps 2;

QY 1 QVQLQESGAEIVRSGASVNLSTCTASGFINIKDYMEHWKQRPREGLEWIGYIDPESGTEY 60
DB 1 QVQLQESGAEIVRSGASVNLSTCTASGFINIKDYMEHWKQRPREGLEWIGYIDPESGTEY 60
QY 61 APNFOGKATVTADTSSNTAYIHLSLTSEDTTVYYCNNAVITYEYDG---YALDIWQGGTT 117
DB 61 APNFOGKATVTADTSSNTAYIHLSLTSEDTTVYYCNNAVITYEYDG---YALDIWQGGTT 117
QY 61 NEKPKRATLTVDKPSSTAYWQLSLTSEDAVYYC-----ARYDGSSEFYMDYWGQSTS 115
DB 61 NEKPKRATLTVDKPSSTAYWQLSLTSEDAVYYC-----ARYDGSSEFYMDYWGQSTS 115
QY 118 VTSSS 122
DB 118 VTSSS 120
QY 116 VTSSS 120
DB 116 VTSSS 120

RESULT 13
Q8KOF2 PRELIMINARY; PRT; 488 AA.
ID Q8KOF2
AC Q8KOF2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

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DE Similar to expressed sequence A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031703; AAH31703.1; -.
DR InterPro; IPR007110; Ig-cl.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR03006; IGMHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IGMHC; 2.
DR SEQUENCE 488 AA; 53127 MW; 0E3B156E15733F0 CRC64;
SQ

Query Match 31.3%; Score 411; DB 11; Length 488;
Best Local Similarity 42.3%; Pred. No. 3.1e-25;
Matches 88; Conservative 24; Mismatches 52; Indels 44; Gaps 4;

QY 1 QVQLQESGAEIVRSGASVNLSTCTASGFINIKDYMEHWKQRPREGLEWIGYIDPESGTEY 60
DB 20 QVQLQESGAEIVRSGASVNLSTCTASGFINIKDYMEHWKQRPREGLEWIGYIDPESGTEY 79
QY 61 APNFOGKATVTADTSSNTAYIHLSLTSEDTTVYYC--NAVITYEYDGALDIWQGGTTV 118
DB 61 NEKPKRATLTVDKPSSTAYWQLSLTSEDAVYYCTRGGLFYSVDYSPMDYWGQSTS 139
QY 119 TVSSG-----GGSGGGSGGGSGD--ELTQSPSS 147
DB 140 TVSSG-----GGSGGGSGGGSGD--ELTQSPSS 149
QY 148 LAVSAGEKIVAMS-----CKSSQSL 166
DB 200 LAVSAGEKIVAMS-----CKSSQSL 225

RESULT 14
Q924Q9 PRELIMINARY; PRT; 145 AA.
ID Q924Q9
AC Q924Q9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE V0186.2-D-J-C-mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067791; BAB63276.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.

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DR PIR; PH1128; PH1128.  
 DR PIR; PH1129; PH1129.  
 DR PIR; PH1131; PH1131.  
 DR PIR; PH1133; PH1133.  
 DR PIR; PH1137; PH1137.  
 DR PIR; PH1139; PH1139.  
 DR PIR; PH1142; PH1142.  
 DR PIR; PH1144; PH1144.  
 DR PIR; PH1147; PH1147.  
 DR PIR; PH1149; PH1149.  
 DR PIR; PH1150; PH1150.  
 DR PIR; PH1151; PH1151.  
 DR PIR; PH1152; PH1152.  
 DR PIR; PH1153; PH1153.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PS50835; Ig\_Like; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 145 145  
 SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match 31.0%; Score 408; DB 11; Length 145;  
 Best Local Similarity 63.9%; Pred. No. 1.2e-25;  
 Matches 78; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVRGASVNI SCTASGFNFKDYMMHWKORPEGLFMIGYIDPESGETEY 60  
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
 1 QVQLQSGAEIVRGASVNI SCTASGFNFKDYMMHWKORPEGLFMIGYIDPESGETEY 60  
 Db  
 QY 61 APNFGKATVYADTSNTAYLHLSITSEDTTVYVCNAVYYEYDGYALDYWGQGTTLTV 120  
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
 61 NEKFKSKATLVTKPSTAYMQLSITSEDSAVYYCARSLITY--YANDYWGQGTTLTV 118  
 Db  
 QY 121 SS 122  
 ||  
 Db 119 SS 120

RESULT 15  
 ID Q924R8 PRELIMINARY; PRT; 146 AA.  
 AC Q924R8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE VHA166-2-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBL\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)";  
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB067781; BAB63266.1; -.  
 DR PIR; F28833; F28833.  
 DR PIR; PH1105; PH1105.  
 DR PIR; PH1108; PH1108.  
 DR PIR; PH1114; PH1114.  
 DR PIR; PH1118; PH1118.  
 DR PIR; PH1119; PH1119.  
 DR PIR; PH1125; PH1125.  
 DR PIR; PH1126; PH1126.  
 DR PIR; PH1128; PH1128.  
 DR PIR; PH1129; PH1129.  
 DR PIR; PH1131; PH1131.  
 DR PIR; PH1134; PH1134.

DR PIR; PH1137; PH1137.  
 DR PIR; PH1139; PH1139.  
 DR PIR; PH1142; PH1142.  
 DR PIR; PH1144; PH1144.  
 DR PIR; PH1147; PH1147.  
 DR PIR; PH1149; PH1149.  
 DR PIR; PH1150; PH1150.  
 DR PIR; PH1151; PH1151.  
 DR PIR; PH1152; PH1152.  
 DR PIR; PH1153; PH1153.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PS50835; Ig\_Like; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16216 MW; 92460F1DFB7538 CRC64;

Query Match 30.9%; Score 406.5; DB 11; Length 146;  
 Best Local Similarity 64.8%; Pred. No. 1.6e-25;  
 Matches 79; Conservative 12; Mismatches 30; Indels 1; Gaps 1;

QY 1 QVQLQSGAEIVRGASVNI SCTASGFNFKDYMMHWKORPEGLFMIGYIDPESGETEY 60  
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
 1 QVQLQSGAEIVRGASVNI SCTASGFNFKDYMMHWKORPEGLFMIGYIDPESGETEY 60  
 Db  
 QY 61 APNFGKATVYADTSNTAYLHLSITSEDTTVYVCNAVYYEYDGYALDYWGQGTTLTV 120  
 ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|  
 61 NEKFKSKATLVTKPSTAYMQLSITSEDSAVYYC-ASYYGSSLYYFDYWGQGTTLTV 119  
 Db  
 QY 121 SS 122  
 ||  
 Db 120 SS 121

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 Job time : 36.4268 sec

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